

Asp	Pro	Ala	Asn	Thr	His	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	385	390	395	400
Glu	Phe	Thr	Glu	Asp	Ala	Ala	Glu	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	405	410	415	
Phe	Gln	Asn	Leu	Phe	Lys	Arg	Leu	Ser	Glu	Lys	Leu	Leu	Trp	Leu	Tyr	420	425	430	
Gln	Glu	Val	Glu	Arg	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	435	440	445	
Arg	Gly	Val	Arg	Leu	Asp	Val	Pro	Leu	Leu	Glu	Ala	Leu	Ser	Phe	Glu	450	455	460	
Leu	Glu	Lys	Glu	Met	Glu	Arg	Leu	Glu	Gly	Glu	Val	Phe	Arg	Leu	Ala	465	470	475	480
Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	485	490	495	
Phe	Asp	Glu	Leu	Gly	Leu	Thr	Pro	Val	Lys	Arg	Thr	Lys	Lys	Thr	Gly	500	505	510	
Lys	Arg	Ser	Thr	Ala	Gln	Gly	Ala	Leu	Glu	Ala	Leu	Arg	Gly	Ala	His	515	520	525	
Pro	Ile	Val	Glu	Leu	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Ser	Lys	Leu	Lys	530	535	540	
Ser	Thr	Tyr	Leu	Asp	Pro	Leu	Pro	Arg	Leu	Val	His	Pro	Arg	Thr	Gly	545	550	555	560
Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	565	570	575	
Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	580	585	590	
Gly	Gln	Arg	Ile	Arg	Lys	Ala	Phe	Val	Ala	Glu	Glu	Gly	Trp	Leu	Leu	595	600	605	
Leu	Ala	Ala	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	610	615	620	
Ser	Gly	Asp	Glu	Asn	Leu	Lys	Arg	Val	Phe	Arg	Glu	Gly	Lys	Asp	Ile	625	630	635	640
His	Thr	Glu	Thr	Ala	Ala	Trp	Met	Phe	Gly	Leu	Asp	Pro	Ala	Leu	Val	645	650	655	
Asp	Pro	Lys	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	660	665	670	
Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Gly	Ile	Asp	Tyr	675	680	685	
Lys	Glu	Ala	Glu	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	690	695	700	
Val	Arg	Ala	Trp	Ile	Glu	Arg	Thr	Leu	Glu	Glu	Gly	Arg	Thr	Arg	Gly	705	710	715	720

Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala  
                     725                    730                    735  
 Ser Arg Val Arg Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
                     740                    745                    750  
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Ile Ala Met Val  
                     755                    760                    765  
 Lys Leu Phe Pro Arg Leu Lys Pro Leu Gly Ala His Leu Leu Leu Gln  
                     770                    775                    780  
 Val Ala Asn Glu Leu Val Leu Glu Val Pro Glu Asp Arg Ala Glu Glu  
                     785                    790                    795                    800  
 Ala Lys Ala Leu Val Lys Glu Val Met Glu Asn Ala Tyr Pro Leu Asp  
                     805                    810                    815  
 Val Pro Leu Glu Val Glu Val Gly Val Gly Arg Asp Trp Leu Glu Ala  
                     820                    825                    830  
 Lys Gln Asp  
                     835

<210> 360

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 360

gggcttcccg ccatcaagaa gacgaagaag acgggcaagc gc

42

<210> 361

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 361

gcgcttgccc gtcttcttcg tcttcttgat ggcgggaagc cc

42

<210> 362  
 <211> 33  
 <212> DNA  
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 <220>  
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 <210> 363  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Synthetic  
 <400> 363  
 gaggaccagt tcgttggcca cctgcaaaag cat 33  
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 <211> 2496  
 <212> DNA  
 <213> Artificial Sequence  
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 <223> Synthetic  
 <400> 364  
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 caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg 180  
 gtgatcgtgg tgtttgacgc caaggccccc tccttcgcgc accagaccta cgaggcctac 240  
 aaggcggggc gggctccac ccccgaggac tttccccggc agcttgccct tatcaaggag 300  
 atggtggacc ttttgggcct ggagcgcctc gaggtgccgg gctttgaagc ggatgacgtc 360  
 ctggctaccc tggccaagaa ggcggaagaa gaaggctacg aagtgcgcac cctcaccgcg 420  
 gaccgggacc tttaccagct tctttcggag cgaatctcca tccttcaccc ggaggggttac 480  
 ctgatcacc cggagtggct ttgggagaag tatgggctta agccttccca gtgggtggac 540  
 taccgggcct tggccgggga cccttcgcac aacatccccg gcgtgaaggg catcggggag 600

aagacggcgg	ccaagctgat	ccgggagtg	ggaagcctgg	aaaaccttct	taagcacctg	660
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ctatccctgg	agctatcccc	ggtgcacacg	gacttgctcc	ttcaggtgga	cttcgccccg	780
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gcggccaaga	ccatcaactt	cggcgtcctc	tacggcatgt	ccgcccaccg	gctttcgggg	2040
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cccaaggtgc	gggcctggat	tgagaaaacc	ctggcggaag	gacgggaacg	gggctatgtg	2160
gaaacctct	ttggccgcg	gcgctacgtg	cccgaacttg	cttcccgggt	gaagagcatc	2220
cgggaggcag	cggagcgcat	ggccttcaac	atgccggctc	aggggaccgc	cgcggatttg	2280
atgaaactgg	ccatggtgaa	gctctttccc	aggcttcagg	agctgggggc	caggatgctt	2340



ttgcaggtgc acaacgaact ggtcctcgag gctcccaagg agcaagcgga ggaagtcgcc 2400  
caggaggcca agcggaccat ggaggaggtg tggcccctga aggtgccctt ggaggtggaa 2460  
gtgggcatcg gggaggactg gctttccgcc aaggcc 2496

<210> 365

<211> 832

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 365

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	1	5	10	15
Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu	20	25	30	
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys	35	40	45	
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val	50	55	60	
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr	65	70	75	80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala	85	90	95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu	Val	100	105	110	
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala	115	120	125	
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu	130	135	140	
Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly	Tyr	145	150	155	160
Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys	Pro	Ser	165	170	175	
Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn	Ile	180	185	190	
Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	Leu	Ile	Arg	195	200	205	
Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu	Glu	Gln	Val	Lys	210	215	220	

Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met Glu Asp Leu Lys  
 225 230 235 240  
 Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu Leu Leu Gln Val  
 245 250 255  
 Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe  
 260 265 270  
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
 275 280 285  
 Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
 290 295 300  
 Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu  
 305 310 315 320  
 Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val Tyr Arg Ala Glu  
 325 330 335  
 Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu Leu  
 340 345 350  
 Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu Ala  
 355 360 365  
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380  
 Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 385 390 395 400  
 Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala Leu  
 405 410 415  
 Leu Lys Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu  
 420 425 430  
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445  
 Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val Glu  
 450 455 460  
 Ala Glu Ile Arg Arg Phe Glu Glu Glu Val His Arg Leu Ala Gly His  
 465 470 475 480  
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Ile Phe Asp  
 485 490 495  
 Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Arg Lys Thr Gly Lys Arg  
 500 505 510  
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
 515 520 525  
 Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly Thr  
 530 535 540  
 Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg Leu  
 545 550 555 560



<400> 366  
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ccggtgcaga tgggtctacg ctctgcccgg agcctcctca aggccttgaa ggaggacgga 180  
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<210> 367

<211> 835

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 367

Met	Asn	Ser	Thr	Pro	Leu	Phe	Asp	Leu	Glu	Glu	Pro	Pro	Lys	Arg	Val
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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Tyr	Ala	Leu
			20					25					30		
Ser	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Met	Val	Tyr	Gly	Phe
		35				40					45				
Ala	Arg	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Gln	Ala	Val	Val
	50				55					60					
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu
65				70					75					80	
Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
			85					90						95	
Leu	Ala	Leu	Val	Lys	Arg	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
		100					105					110			
Glu	Ala	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Gly	Thr	Leu	Ala	Lys
	115					120						125			
Lys	Ala	Glu	Arg	Glu	Gly	Met	Glu	Val	Arg	Ile	Leu	Thr	Gly	Asp	Arg
	130					135					140				

Asp Phe Phe Gln Leu Leu Ser Glu Lys Val Ser Val Leu Leu Pro Asp  
 145 150 155 160  
 Gly Thr Leu Val Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly Val Pro  
 165 170 175  
 Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg Ser Asp  
 180 185 190  
 Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu Arg Leu  
 195 200 205  
 Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu Glu Asp  
 225 230 235 240  
 Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu Pro Leu  
 245 250 255  
 Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly  
 260 265 270  
 Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro  
 290 295 300  
 Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro  
 305 310 315 320  
 Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly Arg Val  
 325 330 335  
 His Arg Ala Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala  
 340 345 350  
 Arg Gly Phe Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly  
 355 360 365  
 Val Ala Leu Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ala Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Phe Thr Glu Asp Ala Ala Glu Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 Phe Gln Asn Leu Phe Lys Arg Leu Ser Glu Lys Leu Leu Trp Leu Tyr  
 420 425 430  
 Gln Glu Val Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
 435 440 445  
 Arg Gly Val Arg Leu Asp Val Pro Leu Leu Glu Ala Leu Ser Phe Glu  
 450 455 460  
 Leu Glu Lys Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala  
 465 470 475 480

Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
 485 490 495  
 Phe Asp Glu Leu Gly Leu Thr Pro Val Lys Arg Thr Lys Lys Thr Gly  
 500 505 510  
 Lys Arg Ser Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His  
 515 520 525  
 Pro Ile Val Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys  
 530 535 540  
 Ser Thr Tyr Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly  
 545 550 555 560  
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
 565 570 575  
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu  
 580 585 590  
 Gly Gln Arg Ile Arg Lys Ala Phe Val Ala Glu Glu Gly Trp Leu Leu  
 595 600 605  
 Leu Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
 610 615 620  
 Ser Gly Asp Glu Asn Leu Lys Arg Val Phe Arg Glu Gly Lys Asp Ile  
 625 630 635 640  
 His Thr Glu Thr Ala Ala Trp Met Phe Gly Leu Asp Pro Ala Leu Val  
 645 650 655  
 Asp Pro Lys Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
 660 665 670  
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Gly Ile Asp Tyr  
 675 680 685  
 Lys Glu Ala Glu Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
 690 695 700  
 Val Arg Ala Trp Ile Glu Arg Thr Leu Glu Glu Gly Arg Thr Arg Gly  
 705 710 715 720  
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala  
 725 730 735  
 Ser Arg Val Arg Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
 740 745 750  
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Ile Ala Met Val  
 755 760 765  
 Lys Leu Phe Pro Arg Leu Lys Pro Leu Gly Ala His Leu Leu Leu Gln  
 770 775 780  
 Val Ala Asn Glu Leu Val Leu Glu Val Pro Glu Asp Arg Ala Glu Glu  
 785 790 795 800

Ala	Lys	Ala	Leu	Val	Lys	Glu	Val	Met	Glu	Asn	Ala	Tyr	Pro	Leu	Asp
				805					810					815	
Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Val	Gly	Arg	Asp	Trp	Leu	Glu	Ala
			820					825					830		

Lys Gln Asp  
835

<210> 368

<211> 2496

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 368

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cagacggcca gctggatggt cggcgtgccc ccagaggccg tggattccct gatgcgccgg	1980
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<210> 369

<211> 832

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 369

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	1	5	10	15
Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu	20	25	30	
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys	35	40	45	
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val	50	55	60	
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr	65	70	75	80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala	85	90	95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	Glu	Val	100	105	110	
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala	115	120	125	
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu	130	135	140	
Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly	Tyr	145	150	155	160
Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys	Pro	Ser	165	170	175	
Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn	Ile	180	185	190	
Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	Leu	Ile	Arg	195	200	205	
Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu	Glu	Gln	Val	Lys	210	215	220	
Pro	Ala	Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met	Glu	Asp	Leu	Lys	225	230	235	240
Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	His	Thr	Asp	Leu	Leu	Leu	Gln	Val	245	250	255	
Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Lys	Ala	Phe	260	265	270	
Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu	275	280	285	
Glu	Ser	Pro	Val	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	290	295	300	
Ala	Phe	Val	Gly	Tyr	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	305	310	315	320

Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val Tyr Arg Ala Glu  
 325 330 335  
 Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu Leu  
 340 345 350  
 Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu Ala  
 355 360 365  
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380  
 Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 385 390 395 400  
 Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala Leu  
 405 410 415  
 Leu Lys Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu  
 420 425 430  
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445  
 Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val Glu  
 450 455 460  
 Ala Glu Ile Arg Arg Phe Glu Glu Glu Val His Arg Leu Ala Gly His  
 465 470 475 480  
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Ile Phe Asp  
 485 490 495  
 Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Arg Lys Thr Gly Lys Arg  
 500 505 510  
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
 515 520 525  
 Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly Thr  
 530 535 540  
 Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg Leu  
 545 550 555 560  
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
 565 570 575  
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 580 585 590  
 Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val Val  
 595 600 605  
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 610 615 620  
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His Thr  
 625 630 635 640  
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Ser  
 645 650 655

Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly  
                   660                                  665                                  670  
 Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu Glu  
                   675                                  680                                  685  
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val Arg  
                   690                                  695                                  700  
 Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr Val  
                   705                                  710                                  715                                  720  
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser Arg  
                                   725                                  730                                  735  
 Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
                                   740                                  745                                  750  
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu  
                                   755                                  760                                  765  
 Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val His  
                   770                                  775                                  780  
 Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val Ala  
                   785                                  790                                  795                                  800  
 Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val Pro  
                                   805                                  810                                  815  
 Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Ala  
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<210> 370

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 370

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33

<210> 371

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 371	
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gaaccgggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
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cccgagggcc acctcatcac ccgggagtgg ctttgggaga agtacggcct caggccggag	540
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caccac						2526
<210> 374						
<211> 842						
<212> PRT						

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 374

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65					70					75					80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
				85					90					95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
			100					105					110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
	130					135					140				
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His
145					150				155						160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly
				165					170					175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro
			180					185					190		
Ser	Asp	Asn	Leu	Ala	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu
		195					200					205			
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu
	210					215					220				
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu
225					230					235					240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu
				245					250					255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly
			260					265					270		
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu
		275					280					285			

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
290 295 300  
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
305 310 315 320  
Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
325 330 335  
His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
340 345 350  
Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
355 360 365  
Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
370 375 380  
Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
385 390 395 400  
Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
405 410 415  
His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
420 425 430  
Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
435 440 445  
Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
450 455 460  
Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
465 470 475 480  
Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
485 490 495  
Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
500 505 510  
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
515 520 525  
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
530 535 540  
Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
545 550 555 560  
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
565 570 575  
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
580 585 590  
Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
595 600 605  
Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
610 615 620



His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
 805 810 815  
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
 820 825 830  
 Ser Ala Lys Gly His His His His His His  
 835 840

<210> 375

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 375

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcgg ccacgaggcc	240

tacgaggcct acaaggcggg gagggccccc acccccgagg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgaggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaag aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgcga cctctaccaa ctcgctctccg accgcgtcgc cgtcctccac	480
cccaggggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcgtaggg gacccctccg acaacctcaa ggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg	780
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Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	

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Leu	Lys	Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	545	550	555	560

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Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	660	665	670
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Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	705	710	715
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Leu	Asn	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	740	745	750
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Glu	Glu	Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	805	810	815
Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	820	825	830
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Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	
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Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	
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Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly
385					390					395					400
Glu	Trp	Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu
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His	Arg	Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp
			420					425					430		
Leu	Tyr	His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met
		435					440					445			
Glu	Ala	Thr	Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser
	450					455					460				
Leu	Glu	Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg
465					470					475					480
Leu	Ala	Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg
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			500					505					510		
Thr	Gly	Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu
		515					520					525			
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<211> 842

<212> PRT

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<220>

<223> Synthetic

<400> 396

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Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	180	185	190	
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	195	200	205	
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	210	215	220	

Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	225	230	235	240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	His	Thr	Asp	Leu	245	250	255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	260	265	270	
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	275	280	285	
Phe	Gly	Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro	290	295	300	
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	305	310	315	320
Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Gly	Gly	Arg	Val	325	330	335	
His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	340	345	350	
Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	355	360	365	
Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	370	375	380	
Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	385	390	395	400
Glu	Trp	Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	405	410	415	
His	Arg	Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp	420	425	430	
Leu	Tyr	His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	435	440	445	
Glu	Ala	Thr	Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	450	455	460	
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Leu	Ala	Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	485	490	495	
Val	Leu	Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Lys	Lys	Thr	Lys	Lys	500	505	510	
Thr	Gly	Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	515	520	525	
Ala	His	Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	530	535	540	
Leu	Lys	Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	545	550	555	560

Thr	Gly	Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	565	570	575
Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	580	585	590
Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	595	600	605
Ala	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	610	615	620
His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	625	630	635
Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	645	650	655
Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	660	665	670
Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	675	680	685
Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	690	695	700
Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	705	710	715
Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	725	730	735
Leu	Asn	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	740	745	750
Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	755	760	765
Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	770	775	780
Leu	Gln	Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	785	790	795
Glu	Glu	Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	805	810	815
Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	820	825	830
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<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 400

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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	180	185	190	
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	195	200	205	
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	210	215	220	

Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	225	230	235	240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	His	Thr	Asp	Leu	245	250	255	
Leu	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	260	265	270	
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	275	280	285	
Phe	Gly	Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro	290	295	300	
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	305	310	315	320
Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Gly	Gly	Arg	Val	325	330	335	
His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	340	345	350	
Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	355	360	365	
Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	370	375	380	
Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	385	390	395	400
Glu	Trp	Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	405	410	415	
His	Arg	Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp	420	425	430	
Leu	Tyr	His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	435	440	445	
Glu	Ala	Thr	Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	450	455	460	
Leu	Glu	Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg	465	470	475	480
Leu	Ala	Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	485	490	495	
Val	Leu	Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Lys	Lys	Thr	Lys	Lys	500	505	510	
Thr	Gly	Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	515	520	525	
Ala	His	Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	530	535	540	
Leu	Lys	Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	545	550	555	560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605  
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
 805 810 815  
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
 820 825 830  
 Ser Ala Lys Gly His His His His His His  
 835 840

<210> 401

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 401

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgctcttcgt ggtctttgac gccaaagccc cctccttcct ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccagg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgaggtccc cggtacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg cggaccgga cctctaccaa ctctctccg accgcgtcgc cgtcctccac	480
cccaggggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttcgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg	780
gacctcgccc aggggcgga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840
gagttcgga gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccc ccccgagccc	960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca	1020
gacctcttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttgg cctcgaggga ggggctagac ctctgcccc gggacgacct catgctcctc	1140
gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcgcggcg ctacgggggg	1200
gagtggacgg aggacgccc ccaccgggcc ctctctcgg agaggctcca tcggaacctc	1260
cttaagcgcc tcgaggggga ggagaagctc gtttggctct accacgaggt ggaaaagccc	1320
ctctccccgg tcctggccca tatggaggcc accgggggtac ggcgggacgt ggcctacctt	1380
caggcccttt ccttgagct tgcggaggag atccgccgcc tcgaggagga ggtcttcgc	1440
ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac	1500

gagcttaggc ttcccgctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc 1560  
 gcggtgctgg aggccctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg 1620  
 gagctcacca agctcaagaa cacctacgtg gacccccctcc caagcctcgt ccacccgagg 1680  
 acggggccgcc tccacacccg cttcaaccag acggccacgg ccacgggggag gcttagtagc 1740  
 tccgacccca acctgcagaa catccccgtc cgcacccccct tgggccagag gatccgcccgg 1800  
 gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860  
 cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctctcca ggaggggaag 1920  
 gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccgaggagc cgtggacccc 1980  
 ctgatgcgcc gggcggccaa gacggtgaac ttcggcgtcc tctacggcat gtccgccccat 2040  
 aggctctccc aggagcttgc catccccctac gaggaggcgg tggcctttat agagcgctac 2100  
 ttccaaagct tccccagggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160  
 cggggctacg tggaaacct cttcggaaga aggcgtacg tgcccgacct caacgcccgg 2220  
 gtgaagagcg tcaggagggc cgcggagcgc atggccttca acatgcccggt ccagggcacc 2280  
 gccgcgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340  
 gccgcgatgc tcctccaggt cgccaacgag ctctcctgg agggccccca agcgcggggc 2400  
 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatccccct cgccgtgccc 2460  
 ctggaggtgg aggtggggat gggggaggac tggttttccg ccaagggt 2508

<210> 402

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 402

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65					70					75				80	

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95  
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110  
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125  
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140  
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
145 150 155 160  
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
165 170 175  
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
180 185 190  
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
195 200 205  
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
210 215 220  
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
225 230 235 240  
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
245 250 255  
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
260 265 270  
Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
275 280 285  
Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
290 295 300  
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
305 310 315 320  
Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
325 330 335  
His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
340 345 350  
Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
355 360 365  
Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
370 375 380  
Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
385 390 395 400  
Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Val Trp  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460  
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
 500 505 510  
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540  
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560  
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605  
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
 805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
 820 825 830

Ser Ala Lys Gly  
 835

<210> 403

<211> 66

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

<221> modified\_base

<222> (19)..(51)

<223> The bases in these positions are a synthesis of 91% base shown and 3% all other bases

<400> 403  
 ctccatcgga acctccttaa gcgcctcgag ggggaggaga agctcctttg gctctaccac 60  
 gaggtg 66

<210> 404

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthesis

<400> 404  
 aaggagggttc cgatggag 18



<210> 405

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 405

atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac	60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaggccc cctccttcgc ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccaggg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg ttaccgcgc tcgagggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgga cctctaccaa ctcgcttcgc accgcgtcgc cgtcctccac	480
cccgagggcc acctcatcac ccgggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg	780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840
gagttcggca gcctcctcca cgagttcggc ctctggagg ccccgcccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc	960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgtgca ccgggcagca	1020
gacctcttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttgg cctcgaggga ggggctagac ctcgtgcccc gggacgacct catgctcctc	1140
gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcgcggcg ctacgggggg	1200
gagtggacgg aggacgccgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc	1260
cttaagcgcc tcgagggggg ggagaagctc ctttggctct accacgaggt ggaaaagccc	1320
ctctcccggg tcctggccca tatggaggcc accgggggtac ggcgggacgt ggcctacctt	1380
caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttcgc	1440
ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggt gctctttgac	1500

gagcttaggc ttcccgctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc 1560  
 gcggtgctgg aggccctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg 1620  
 gagctcacca agctcaagaa cacctacgtg gacccccctcc caagcctcgt ccacccgagg 1680  
 acggggccgcc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740  
 tccgacccca acctgcagaa catccccgtc cgcacccccct tgggccagag gatccgccgg 1800  
 gccttcgtgg ccgaggcggg ttgggcgttg gtggcccttg actatagcca gatagagctc 1860  
 cgcgtccteg cccacctctc cggggacgaa aacctgatca gggctctcca ggaggggaag 1920  
 gacatccaca cccagaccgc aagctggatg ttcggcgctc ccccgagggc cgtggacccc 1980  
 ctgatgcgcc gggcgggcaa gacggtgaac ttcggcgctc tctacggcat gtccgcccat 2040  
 aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100  
 ttccaaagct tccccaaagt gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160  
 cggggctacg tggaaacct cttcggaaga aggcgctacg tgcccgacct caacgcccgg 2220  
 gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccggt ccagggcacc 2280  
 gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340  
 gcccgcatgc tctccaggt cgccaacgag ctctcctgg agggccccca agcgcggggc 2400  
 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460  
 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggt 2508

<210> 406

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 406

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65					70					75				80	

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95  
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110  
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125  
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140  
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
145 150 155 160  
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
165 170 175  
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
180 185 190  
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
195 200 205  
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
210 215 220  
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
225 230 235 240  
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
245 250 255  
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
260 265 270  
Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
275 280 285  
Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
290 295 300  
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
305 310 315 320  
Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
325 330 335  
His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
340 345 350  
Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
355 360 365  
Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
370 375 380  
Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
385 390 395 400  
Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Val Glu Lys Leu Leu Trp  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460  
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
 500 505 510  
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540  
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560  
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605  
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750



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<211>	836					
<212>	PRT					

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 408

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Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	
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Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	
	50					55					60					
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	
65					70					75					80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	
				85					90					95		
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	
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Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	
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Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	
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Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	
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Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	
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Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	
		195					200					205				
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	
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Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	
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Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	
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Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	
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Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	
		275					280						285			

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
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Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
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Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
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Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
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Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
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Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
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Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile
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Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe
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Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys
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Leu	Asn	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala
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Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala
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Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu
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Leu	Gln	Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala
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Glu	Glu	Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro
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<211> 2508

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<213> Artificial Sequence

<220>

<223> Synthetic

<400> 409

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<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 410

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Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	

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 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205  
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
 210 215 220  
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
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 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
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 305 310 315 320  
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Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
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 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
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 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
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 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
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<220>

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<210> 412

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 412

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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				

Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	180	185	190	
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	195	200	205	
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	210	215	220	
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	225	230	235	240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	245	250	255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	260	265	270	
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	275	280	285	
Phe	Gly	Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro	290	295	300	
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	305	310	315	320
Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Gly	Gly	Arg	Val	325	330	335	
His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	340	345	350	
Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	355	360	365	
Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	370	375	380	
Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	385	390	395	400



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 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
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 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
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 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
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 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
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 610 615 620  
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 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
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 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
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 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
                     755                    760                    765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
                     770                    775                    780  
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
                     785                    790                    795                    800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
                     805                    810                    815  
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<210> 413

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<220>

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<400> 413

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42

<210> 414

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 414

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18

<210> 415

<211> 2508

<212> DNA

<213> Artificial Sequence

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<223> Synthetic

<400> 415

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<210> 416

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 416

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			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65					70					75				80	

Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95  
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110  
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125  
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140  
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
145 150 155 160  
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
165 170 175  
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
180 185 190  
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
195 200 205  
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
210 215 220  
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
225 230 235 240  
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
245 250 255  
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
260 265 270  
Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
275 280 285  
Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
290 295 300  
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
305 310 315 320  
Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
325 330 335  
His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
340 345 350  
Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
355 360 365  
Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
370 375 380  
Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
385 390 395 400  
Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
405 410 415

His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
                   420                                  425                                  430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
                   435                                  440                                  445

Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
                   450                                  455                                  460

Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465                                  470                                  475                                  480

Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
                                   485                                  490                                  495

Val Leu Phe Asp Glu Leu Arg Leu Pro Val Leu Lys Lys Thr Lys Lys  
                                   500                                  505                                  510

Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
                   515                                  520                                  525

Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
                   530                                  535                                  540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545                                  550                                  555                                  560

Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
                                   565                                  570                                  575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
                                   580                                  585                                  590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
                   595                                  600                                  605

Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
                   610                                  615                                  620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625                                  630                                  635                                  640

Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
                                   645                                  650                                  655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
                                   660                                  665                                  670

Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
                   675                                  680                                  685

Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
                   690                                  695                                  700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705                                  710                                  715                                  720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
                                   725                                  730                                  735

Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
                                   740                                  745                                  750

Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
 805 810 815  
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 820 825 830  
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<210> 417

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 417

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<211>	836					
<212>	PRT					



<213> Artificial Sequence

<220>

<223> Synthetic

<400> 418

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			20					25					30			
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	
		35					40					45				
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	
	50					55					60					
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	
65					70					75					80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	
				85					90					95		
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	
			100					105					110			
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	
		115					120					125				
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	
	130					135					140					
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	
145					150				155						160	
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	
				165					170					175		
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	
			180					185					190			
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	
		195					200					205				
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	
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Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	
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Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	
				245					250					255		
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	
			260					265					270			
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	
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Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
305 310 315 320  
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325 330 335  
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Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
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Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
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Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
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Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
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Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
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Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
610 615 620

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 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
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 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
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 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
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 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
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 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
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 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
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 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
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 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
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 Ser Ala Lys Gly  
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<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 419

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaagccc cctccttcg ccacgaggcc	240

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<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 420

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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	

Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
 180 185 190  
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205  
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
 210 215 220  
 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240  
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255  
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270  
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
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 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
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 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335  
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
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 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
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 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
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 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
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 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
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 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
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 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
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 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
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Thr Gly Lys Arg Ser Thr Gly Ala Ala Val Leu Glu Ala Leu Arg Glu  
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 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
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 Ser Ala Lys Gly  
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<211> 836

<212> PRT

<213> Artificial Sequence

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<223> Synthetic

<400> 424

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
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Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	180	185	190	
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	195	200	205	

Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
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 Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
 225 230 235 240  
 Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255  
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270  
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300  
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320  
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335  
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350  
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365  
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460  
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
 500 505 510  
 Thr Gly Lys Arg Ser Thr Ser Leu Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540

Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560  
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605  
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
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 Ser Ala Lys Gly  
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<210> 425  
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 gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180  
 ggggtacaagg ccgtcttcgt ggtctttgac gccaaggccc cctccttcgg ccacgaggcc 240  
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 ggcacgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660  
 ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720  
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atgtgggchg agcttaaagc cctggccgcc tgcaggggch gccgcgtgca ccgggcagca	1020
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gccgtcttgg cctcgaggga ggggctagac ctctgcccc gggacgacct catgctctc	1140
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gccttcgtgg ccgaggcggt ttgggcgttg gtggccctgg actatagcca gatagagctc	1860
cgcgctctcg cccacctctc cggggacgaa aacctgatca gggcttcca ggaggggaag	1920
gacatccaca cccagaccgc aagctggatg ttcggcgctc ccccgaggc cgtggacccc	1980
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gcccgcacgc tctccaggt cgccaacgag ctctcctgg agggccccca agcgcgggcc	2400
gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc	2460
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<210> 427

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 427

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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	
			20					25					30			
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	
		35					40					45				
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	
	50					55					60					
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	
65					70					75					80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	
				85					90					95		
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	
			100					105					110			
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	
		115					120					125				
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	
	130					135					140					
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	
145					150				155						160	
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	
				165					170					175		
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	
			180					185					190			
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	
		195					200					205				
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	
	210					215					220					
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	
225					230					235					240	
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	
				245					250					255		

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270  
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300  
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320  
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335  
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350  
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365  
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460  
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
 500 505 510  
 Thr Gly Lys Arg Ser Thr Ser Arg Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540  
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560  
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590



Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605  
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
 805 810 815  
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
 820 825 830  
 Ser Ala Lys Gly  
 835

<210> 428

<211> 2499

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 428

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gacgcggtga	tcgtggtcct	tgacgccaag	gccccctcct	tccgccacga	ggcctacggg	240
gggtacaagg	cgggccgggc	ccccacgccg	gaggactttc	cccggcaact	cgccctcatc	300
aaggagctgg	tggacctcct	ggggctggcg	cgctcagagg	tcccgggcta	cgaggcggac	360
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gccgactacc	gggccctgac	cggggacgag	tccgacaacc	ttcccggggg	caagggcatc	600
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gatcttctgg	ccctggccgc	cgccaggggc	ggccgcgtcc	accgggcccc	cgagccttat	1020
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gccctgaggg	aaggccttgg	cctcccgccc	ggcgacgacc	ccatgctcct	cgcctacctc	1140
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gccgaggagg	ggtggctatt	ggtggccctg	gactatagcc	agatagagct	caggggtgctg	1860

gccacacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920  
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 ctcttcagg tgcccaacga gctggtcctc gaggcccca aagagagggc ggaggccgtg 2400  
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<210> 429

<211> 833

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 429

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			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70				75					80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu  
 355 360 365  
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg  
 420 425 430  
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Arg Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val  
 450 455 460  
 Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Gln Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His  
 625 630 635 640  
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 Ala Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val  
 785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val  
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Glu

<210> 430

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 430

acgggggtgc gccgggacgt ggcctat

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<210> 431

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 431

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg cgtcttcgt ggtctttgac gccaaaggccc cctccttcgc ccacgaggcc	240
tacgaggcct acaaggcggg gagggcccg acccccagg acttccccgc gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg ttaccgcgc tcgaggtccc cggtacgag	360
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<210> 432

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 432

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Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	
		35					40					45				
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	
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Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	
65					70					75					80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	
				85					90					95		
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	
		100						105					110			
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	
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Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	
	130					135					140					
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	
145					150				155						160	
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	
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Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	
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Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	
		195					200					205				
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	
	210					215					220					
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	
225					230					235					240	
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	
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Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270  
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300  
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320  
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335  
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350  
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365  
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
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 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
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 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
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 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
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 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Arg Leu Pro Lys Leu Lys Lys Thr Lys Lys  
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 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540  
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
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 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
           595                                  600                                  605  
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
           610                                  615                                  620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
           625                                  630                                  635                                  640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
                                   645                                  650                                  655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
                                   660                                  665                                  670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
                                   675                                  680                                  685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
           690                                  695                                  700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
           705                                  710                                  715                                  720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
                                   725                                  730                                  735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
                                   740                                  745                                  750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
                                   755                                  760                                  765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
           770                                  775                                  780  
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
           785                                  790                                  795                                  800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
                                   805                                  810                                  815  
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
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<210> 433

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 433  
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<210> 436

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 436

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Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45  
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60  
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80  
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95  
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110  
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125  
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140  
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
145 150 155 160  
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
165 170 175  
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
180 185 190  
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
195 200 205  
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
210 215 220  
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
225 230 235 240  
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
245 250 255  
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
260 265 270  
Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
275 280 285

Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
290 295 300  
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
305 310 315 320  
Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
325 330 335  
His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
340 345 350  
Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
355 360 365  
Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
370 375 380  
Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
385 390 395 400  
Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
405 410 415  
His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
420 425 430  
Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
435 440 445  
Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
450 455 460  
Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
465 470 475 480  
Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
485 490 495  
Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
500 505 510  
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
515 520 525  
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
530 535 540  
Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
545 550 555 560  
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
565 570 575  
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
580 585 590  
Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
595 600 605  
Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
610 615 620

His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640  
 Asp Ile Ala Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
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 Ser Ala Lys Gly  
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<210> 437

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 437

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33

<210> 438  
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gcccgcacgc	tcctccaggt	cgccaacgag	ctcctcctgg	aggcccccca	agcgcggg	2400
gaggaggtgg	cggcttttgg	caaggaggcc	atggagaagg	cctatcccct	cgcggtgccc	2460
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<210> 440

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 440

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Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45  
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60  
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80  
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95  
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110  
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125  
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140  
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
145 150 155 160  
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
165 170 175  
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
180 185 190  
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
195 200 205  
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
210 215 220  
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
225 230 235 240  
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
245 250 255  
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
260 265 270  
Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
275 280 285  
Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
290 295 300  
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
305 310 315 320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335  
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350  
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365  
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460  
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Pro Lys Lys  
 500 505 510  
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540  
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560  
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605  
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
 805 810 815  
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
 820 825 830  
 Ser Ala Lys Gly  
 835

<210> 441

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 441

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33

<210> 442

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 442  
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<210> 443

<211> 2499

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 443  
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ccggtgcagg cgggtctacgg ctctgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggccgggc cccacgcgc gaggactttc cccggcaact cgccctcatc 300  
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gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc tcccgggggt caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720  
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aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
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tccctggagg tggaggcgga gataaggcgc ttcgaggagg aggtccaccg cctggccggg 1440  
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<210> 444

<211> 833

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 444

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			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
 50 55 60  
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
 65 70 75 80  
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95  
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu  
 100 105 110  
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val Tyr Arg Ala  
 325 330 335  
 Glu Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Ile Ala Leu  
 355 360 365  
 Ala Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380

Asn Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Tyr Ala Ala  
 405 410 415  
 Leu Leu Lys Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu  
 420 425 430  
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser Leu Glu Val  
 450 455 460  
 Glu Ala Glu Ile Arg Arg Phe Glu Glu Glu Val His Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Ile Phe  
 485 490 495  
 Asp Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Arg Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Gly  
 530 535 540  
 Thr Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys Thr Asn Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Arg Leu Val  
 595 600 605  
 Val Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln Asp Ile His  
 625 630 635 640  
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655  
 Ser Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu Arg Gly Tyr  
 705 710 715 720



Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser  
725 730 735  
Arg Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
740 745 750  
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
755 760 765  
Leu Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu Leu Gln Val  
770 775 780  
His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala Glu Glu Val  
785 790 795 800  
Ala Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro Leu Lys Val  
805 810 815  
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Ala

<210> 445

<211> 2496

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 445

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ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg      180
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gggtacaagg cgggccgggc cccacgccg gaggactttc cccggcaact cgccctcatc      300
aaggagctgg tggacctcct ggggttcacg cgctcgagg tcccgggcta cgaggcggac      360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc      420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag      480
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caagtggcca acgagctggg cctggagggtg cccgaggacc gggccgagga ggccaaggcc	2400
ctggtcaagg aggtcatgga gaacgcctac cccctggacg tgcccctcga ggtggagggtg	2460
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<210> 446

<211> 832

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 446

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20 25 30  
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe  
35 40 45  
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60  
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80  
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95  
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu  
100 105 110  
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125  
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140  
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160  
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175  
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190  
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205  
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220  
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
225 230 235 240  
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
245 250 255

Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
260 265 270  
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
275 280 285  
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
290 295 300  
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
305 310 315 320  
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
325 330 335  
Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala Arg Gly Phe  
340 345 350  
Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Val Ala Leu  
355 360 365  
Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu Asp Pro Ala  
370 375 380  
Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Phe Thr  
385 390 395 400  
Glu Asp Ala Ala Glu Arg Ala Leu Leu Ser Glu Arg Leu Phe Gln Asn  
405 410 415  
Leu Phe Lys Arg Leu Ser Glu Lys Leu Leu Trp Leu Tyr Gln Glu Val  
420 425 430  
Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Arg Gly Val  
435 440 445  
Arg Leu Asp Val Pro Leu Leu Glu Ala Leu Ser Phe Glu Leu Glu Lys  
450 455 460  
Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala Gly His Pro  
465 470 475 480  
Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu  
485 490 495  
Leu Gly Leu Thr Pro Val Lys Arg Thr Lys Lys Thr Gly Lys Arg Ser  
500 505 510  
Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His Pro Ile Val  
515 520 525  
Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys Ser Thr Tyr  
530 535 540  
Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly Arg Leu His  
545 550 555 560  
Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser  
565 570 575  
Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg  
580 585 590

Ile Arg Lys Ala Phe Val Ala Glu Glu Gly Trp Leu Leu Leu Ala Ala  
 595 600 605  
 Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp  
 610 615 620  
 Glu Asn Leu Lys Arg Val Phe Arg Glu Gly Lys Asp Ile His Thr Glu  
 625 630 635 640  
 Thr Ala Ala Trp Met Phe Gly Leu Asp Pro Ala Leu Val Asp Pro Lys  
 645 650 655  
 Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met  
 660 665 670  
 Ser Ala His Arg Leu Ser Gln Glu Leu Gly Ile Asp Tyr Lys Glu Ala  
 675 680 685  
 Glu Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala  
 690 695 700  
 Trp Ile Glu Arg Thr Leu Glu Glu Gly Arg Thr Arg Gly Tyr Val Glu  
 705 710 715 720  
 Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala Ser Arg Val  
 725 730 735  
 Arg Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val  
 740 745 750  
 Gln Gly Thr Ala Ala Asp Leu Met Lys Ile Ala Met Val Lys Leu Phe  
 755 760 765  
 Pro Arg Leu Lys Pro Leu Gly Ala His Leu Leu Leu Gln Val Ala Asn  
 770 775 780  
 Glu Leu Val Leu Glu Val Pro Glu Asp Arg Ala Glu Glu Ala Lys Ala  
 785 790 795 800  
 Leu Val Lys Glu Val Met Glu Asn Ala Tyr Pro Leu Asp Val Pro Leu  
 805 810 815  
 Glu Val Glu Val Gly Val Gly Arg Asp Trp Leu Glu Ala Lys Gln Asp  
 820 825 830

<210> 447

<211> 2508

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 447

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcttcgt ggtctttgac gccaaagccc cctccttcg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccagagg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcc tcgagggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgga cctctaccaa ctctctccg accgcgtcgc cgtcctccac	480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg	780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840
gagttcgga gctcctcca cgagttcggc ctctggagg cccccgcccc cctggaggag	900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccc ccccgagccc	960
atgtgggcgg agcttaaagc cctggccgcc tgcaggggcg gccgcgttta ccgggcggag	1020
gatcccttgg aggccttgcg ggggcttggg gaggtgaggg ggcttttggc caaggacctg	1080
gcggtgctgg ccctgaggga agggattgcc ctggcaccgg gcgacgacct catgctctc	1140
gcctacctcc tggatccttc caacaccgcc cccgaagggg tagcccggcg ctacgggggg	1200
gagtggaccg aggagggggg ggaaagggcg ctgctttccg aaaggcttta cgccgccctc	1260
ctgaagcggc ttaaggggga ggagaggctt ctttggcttt acgaggaggt ggaaaagccc	1320
ctttcgcggg tcctggcca catggaggcc acgggggtac ggttggatgt ggcctactta	1380
aaggcccttt ccctggagg gtgggcggag ataaggcgt tcgaggagga ggtccaccgc	1440
ctggccgggc atcctttcaa cctgaactcc cgggaccagc tggaaagggt catctttgac	1500
gagcttgggc ttcccgccat caagaagacg aggaagacgg gcaagcgctc caccagcgcc	1560
gccgttttgg aggccttgcg ggaggctcat cccatcgtgg accgcatact tcagtaccgg	1620
gagctttcca agctcaaggg aacctacatc gatcccttgc ctgccctggg ccaccccaag	1680
acgaaccgcc tccacaccg tttcaaccag acggccaccg ccacggggag gcttagcagc	1740
tcggatccta atctgcaaaa tatccccgtg cgcaccctt tgggccagcg gatccgcgg	1800
gccttcgtgg ccgaggagg gtggaggctg gtggttttgg actacagcca gattgagctc	1860

agggtcctgg cgcacctttc cggggacgag aacctaatacc gggctctcca ggagggccag 1920  
 gacatccaca cccagacggc cagctggatg ttcggcgtgc cccagagggc cgtggattcc 1980  
 ctgatgcgcc gggcggccaa gaccatcaac ttcggcgtcc tctacggcat gtccgcccac 2040  
 cggctttcgg gagagctggc catcccctac gaggaggcgg tggccttcat cgagcggat 2100  
 ttccagagct accccaaggt gcgggcctgg attgagaaaa ccctggcgga aggacgggaa 2160  
 cggggctatg tggaaaacct ctttggccgc cggcgctacg tgcccgaact ggcttcccgg 2220  
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 gccgcggatt tgatgaaact ggccatggtg aagctctttc ccaggcttca ggagctgggg 2340  
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 gaggaagtcg cccaggaggc caagcggacc atggaggagg tgtggcccct gaaggtgccc 2460  
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<210> 448

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 448

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65				70					75					80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
			85					90						95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
		100						105					110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140  
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
145 150 155 160  
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
165 170 175  
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
180 185 190  
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
195 200 205  
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
210 215 220  
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
225 230 235 240  
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
245 250 255  
Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
260 265 270  
Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
275 280 285  
Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
290 295 300  
Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
305 310 315 320  
Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
325 330 335  
Tyr Arg Ala Glu Asp Pro Leu Glu Ala Leu Arg Gly Leu Gly Glu Val  
340 345 350  
Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly  
355 360 365  
Ile Ala Leu Ala Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
370 375 380  
Asp Pro Ser Asn Thr Ala Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
385 390 395 400  
Glu Trp Thr Glu Glu Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu  
405 410 415  
Tyr Ala Ala Leu Leu Lys Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp  
420 425 430  
Leu Tyr Glu Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
435 440 445  
Glu Ala Thr Gly Val Arg Leu Asp Val Ala Tyr Leu Lys Ala Leu Ser  
450 455 460



Leu Glu Val Glu Ala Glu Ile Arg Arg Phe Glu Glu Glu Val His Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Ile Phe Asp Glu Leu Gly Leu Pro Ala Ile Lys Lys Thr Arg Lys  
 500 505 510  
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Asp Arg Ile Leu Gln Tyr Arg Glu Leu Ser Lys  
 530 535 540  
 Leu Lys Gly Thr Tyr Ile Asp Pro Leu Pro Ala Leu Val His Pro Lys  
 545 550 555 560  
 Thr Asn Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp  
 595 600 605  
 Arg Leu Val Val Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Gln  
 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655  
 Ala Val Asp Ser Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gly Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Tyr  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Ala Glu Gly Arg Glu  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Ala Ser Arg Val Lys Ser Ile Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Gln Glu Leu Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Gln Ala  
 785 790 795 800

Glu Glu Val Ala Gln Glu Ala Lys Arg Thr Met Glu Glu Val Trp Pro  
                     805                    810                    815  
 Leu Lys Val Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu  
                     820                    825                    830  
 Ser Ala Lys Ala  
                     835

<210> 449

<211> 2505

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 449

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gaaccggtgc aggcggtcta cggttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg cagtcttcgt ggtctttgac gccaaaggccc cctccttcgc ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccc acccccaggg acttccccgc gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg ttaccgcgc tcgagggtccc cggtacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgagggtgcgc	420
atcctcaccg ccgaccgoga cctctaccaa ctcgctctcc accgcgtcgc cgtcctccac	480
cccagaggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttcgcgc cctcgtgggg gaccctccg acaacctccc cgggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg	720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg	780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg	840
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gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccc ccccagcccc	960
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agcccggttg aggcctggc cgacctcaag gagggccggg ggttcctggc caaggacctg	1080
gccgttttgg ccctgcggga gggggtggcc ctggaccca cgacgaccc cctcctggtg	1140
gcctacctcc tggaccggc caacaccac cccgaggggg tggcccggc ctacgggggc	1200

gagttcacgg aggacgcagc ggagagggcc ctctctccg agaggctctt ccagaacctc	1260
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ctctcctttg agctggagaa ggagatggag cgcctggagg gggaggctctt ccgtttggcc	1440
ggccacccct tcaacctcaa ctcccgcgac cagctggaaa gggtcctctt tgacgagctg	1500
ggcctcacc cgggtgaagcg gacgaagaag acgggcaagc gctccaccgc ccagggggcc	1560
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tccaagctca aaagcaccta cctggacccc ctgccccggc tcgtccacc gcggacgggc	1680
cggctccaca cccgcttcaa ccagacggcc acggccacgg gaaggctttc cagctccgac	1740
cccaacctgc agaacatccc cgtgcgcacc cccttggggc agcgcacccg caaggccttc	1800
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ctggcccacc tctcggggga cgagaacctg aagcgggtct tccgggaggg gaaggacatc	1920
cataccgaga ccgcgcctg gatgttcggc ttagaccccg ctctggtgga tccaaagatg	1980
cgcggggcgg ccaagacggc caacttcggc gtctctacg ggatgtccgc ccacaggctc	2040
tccaggagc tcggcataga ctacaaggag gcggaggcct ttattgagcg ctacttccag	2100
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ctctcctcc aagtggccaa cgagctggc ctggaggctc ccgaggaccg ggccgaggag	2400
gccaaaggccc tggatcaagga ggtcatggag aacgcctacc ccctggacgt gcccctcgag	2460
gtggagggtg gcgtgggtcg ggactggctg gaggcgaagc aggat	2505

<210> 450

<211> 835

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 450

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
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Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155	160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	180	185	190	
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	195	200	205	
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	210	215	220	
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	225	230	235	240
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	245	250	255	
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	260	265	270	
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	275	280	285	
Phe	Gly	Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro	290	295	300	
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	305	310	315	320

Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335  
 His Arg Ala Thr Ser Pro Val Glu Ala Leu Ala Asp Leu Lys Glu Ala  
 340 345 350  
 Arg Gly Phe Leu Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly  
 355 360 365  
 Val Ala Leu Asp Pro Thr Asp Asp Pro Leu Leu Val Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ala Asn Thr His Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Phe Thr Glu Asp Ala Ala Glu Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 Phe Gln Asn Leu Phe Lys Arg Leu Ser Glu Lys Leu Leu Trp Leu Tyr  
 420 425 430  
 Gln Glu Val Glu Arg Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
 435 440 445  
 Arg Gly Val Arg Leu Asp Val Pro Leu Leu Glu Ala Leu Ser Phe Glu  
 450 455 460  
 Leu Glu Lys Glu Met Glu Arg Leu Glu Gly Glu Val Phe Arg Leu Ala  
 465 470 475 480  
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
 485 490 495  
 Phe Asp Glu Leu Gly Leu Thr Pro Val Lys Arg Thr Lys Lys Thr Gly  
 500 505 510  
 Lys Arg Ser Thr Ala Gln Gly Ala Leu Glu Ala Leu Arg Gly Ala His  
 515 520 525  
 Pro Ile Val Glu Leu Ile Leu Gln Tyr Arg Glu Leu Ser Lys Leu Lys  
 530 535 540  
 Ser Thr Tyr Leu Asp Pro Leu Pro Arg Leu Val His Pro Arg Thr Gly  
 545 550 555 560  
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
 565 570 575  
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu  
 580 585 590  
 Gly Gln Arg Ile Arg Lys Ala Phe Val Ala Glu Glu Gly Trp Leu Leu  
 595 600 605  
 Leu Ala Ala Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
 610 615 620  
 Ser Gly Asp Glu Asn Leu Lys Arg Val Phe Arg Glu Gly Lys Asp Ile  
 625 630 635 640  
 His Thr Glu Thr Ala Ala Trp Met Phe Gly Leu Asp Pro Ala Leu Val  
 645 650 655

Asp Pro Lys Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
 660 665 670  
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Gly Ile Asp Tyr  
 675 680 685  
 Lys Glu Ala Glu Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
 690 695 700  
 Val Arg Ala Trp Ile Glu Arg Thr Leu Glu Glu Gly Arg Thr Arg Gly  
 705 710 715 720  
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Ala  
 725 730 735  
 Ser Arg Val Arg Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
 740 745 750  
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Ile Ala Met Val  
 755 760 765  
 Lys Leu Phe Pro Arg Leu Lys Pro Leu Gly Ala His Leu Leu Leu Gln  
 770 775 780  
 Val Ala Asn Glu Leu Val Leu Glu Val Pro Glu Asp Arg Ala Glu Glu  
 785 790 795 800  
 Ala Lys Ala Leu Val Lys Glu Val Met Glu Asn Ala Tyr Pro Leu Asp  
 805 810 815  
 Val Pro Leu Glu Val Glu Val Gly Val Gly Arg Asp Trp Leu Glu Ala  
 820 825 830  
 Lys Gln Asp  
 835

<210> 451

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 451

cttctctcat cgcgcaaaac agcc

24

<210> 452

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 452  
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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180  
gggtacaagg ccgtcatcgt ggtctttgac gccgaggccc cctccttcg ccacgaggcc 240  
tacgaggcct acaaggcggg gagggccccg acccccagagg acttcccccg gcagctcgcc 300  
ctcatcaagg agctggtgga cctcctgggg tttaccgccg tcgagggtccc cggtacgag 360  
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgagggtgcgc 420  
atcctcaccg ccgaccgcga cctctaccaa ctctgtctcg accgcgtcgc cgtcctccac 480  
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540  
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Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
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Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
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Glu	Asp	Leu	Lys	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	His	Thr	Asp	Leu	245	250	255	
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Phe	Gly	Leu	Leu	Glu	Ser	Pro	Val	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	290	295	300	
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Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
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Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
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Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
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625 630 635 640  
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645 650 655

Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
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 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
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 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
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 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460  
 ctggaggtgg aggtggggat gggggaggac tggttttccg ccaagggtca ccaccaccac 2520  
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<210> 460

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 460

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			



Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	
50						55					60					
Val	Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	
65				70						75					80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	
				85					90					95		
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	
			100					105					110			
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	
		115					120					125				
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	
	130					135					140					
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	
145					150					155					160	
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	
				165					170					175		
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	
			180					185					190			
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	
		195					200					205				
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu	
	210					215					220					
Glu	Gln	Val	Lys	Pro	Ala	Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met	
225					230					235					240	
Glu	Asp	Leu	Lys	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	His	Thr	Asp	Leu	
				245					250					255		
Leu	Leu	Gln	Val	Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	
			260				265						270			
Leu	Lys	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	
		275					280					285				
Phe	Gly	Leu	Leu	Glu	Ser	Pro	Val	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	
	290					295					300					
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Tyr	Val	Leu	Ser	Arg	Pro	Glu	Pro	
305					310					315					320	
Met	Trp	Ala	Glu	Leu	Asn	Ala	Leu	Ala	Ala	Ala	Trp	Gly	Gly	Arg	Val	
				325					330					335		
His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	
			340					345					350			
Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	
		355					360					365				
Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	
	370					375					380					

Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	385	390	395	400
Glu	Trp	Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	405	410	415	
His	Arg	Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp	420	425	430	
Leu	Tyr	His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	435	440	445	
Glu	Ala	Thr	Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	450	455	460	
Leu	Glu	Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg	465	470	475	480
Leu	Ala	Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	485	490	495	
Val	Leu	Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Lys	Lys	Thr	Lys	Lys	500	505	510	
Thr	Gly	Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	515	520	525	
Ala	His	Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	530	535	540	
Leu	Lys	Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	545	550	555	560
Thr	Gly	Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	565	570	575	
Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	580	585	590	
Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	595	600	605	
Ala	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	610	615	620	
His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	625	630	635	640
Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	645	650	655	
Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	660	665	670	
Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	675	680	685	
Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	690	695	700	
Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	705	710	715	720

Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
                             725                            730                            735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
                             740                            745                            750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
                             755                            760                            765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
                             770                            775                            780  
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
                             785                            790                            795                            800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
                             805                            810                            815  
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
                             820                            825                            830  
 Ser Ala Lys Gly His His His His His His  
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<210> 461

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 461  
 gtccaggttc ttgaggaggt tttccag

27

<210> 462

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 462  
 ctctcaaga acctggaccg ggtaaag

27

<210> 463

<211> 2532

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 463

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ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc	120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcatcgt ggtctttgac gccgaggccc cctccttccg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccagagg acttcccccg gcagctcgcc	300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgagggtccc cggctacgag	360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgcga cctctaccaa ctctgtctccg accgcgtcgc cgtcctccac	480
cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag	540
cagtgggtgg acttccgcgc cctcgtgggg gacccctccg acaacctccc cgggggtcaag	600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc	660
ctcaagaacc tggaccgggt aaagccggac tcgctccggc gcaagataga ggcgacctc	720
gaggacctcc acctctcctt agacctggcc cgcctccgca ccgacctccc cctggagggtg	780
gactttaagg ccctgcgccg caggaccccc gacctggagg gcctgagggc ctttttggag	840
gagctggagt tcggaagcct cctccacgag ttcggcctcc tgggagggga gaagccccgg	900
gaggaggccc cctggccccg gcccgagggt gccttcgtgg gcttctcctt ttcccgcaag	960
gagcccatgt gggcgagct tctggccctg gcggcgccct cgggcggccg cgtgcaccgg	1020
gcagcagacc ccttggcggg gctaaaggac ctcaaggagg tccggggcct cctcgccaag	1080
gacctcgccg tcttggcctc gagggagggg ctagacctcg tgcccgggga cgaccccatg	1140
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taccttcagg ccctttccct ggagcttgcg gaggagatcc gccgcctcga ggaggaggtc	1440
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 gcccgggtga agagcgtcag ggaggccgcg gagcgcatgg ccttcaacat gcccgccag 2280  
 ggcaccgccg ccgacctcat gaagctcgcc atggtgaagc ttttcccccg cctccgggag 2340  
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 cggggccgagg aggtggcggc tttggccaag gaggccatgg agaaggccta tcccctcgcc 2460  
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 caccaccacc ac 2532

<210> 464

<211> 844

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 464

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
65				70						75				80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
				85					90					95	

Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
 100 105 110  
 Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
 115 120 125  
 Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
 130 135 140  
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
 145 150 155 160  
 Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
 165 170 175  
 Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
 180 185 190  
 Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205  
 Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
 210 215 220  
 Asp Arg Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu  
 225 230 235 240  
 Glu Asp Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu  
 245 250 255  
 Pro Leu Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu  
 260 265 270  
 Glu Gly Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu  
 275 280 285  
 His Glu Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro  
 290 295 300  
 Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys  
 305 310 315 320  
 Glu Pro Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly  
 325 330 335  
 Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys  
 340 345 350  
 Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg  
 355 360 365  
 Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr  
 370 375 380  
 Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr  
 385 390 395 400  
 Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu  
 405 410 415  
 Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu  
 420 425 430

Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala  
 435 440 445  
 His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala  
 450 455 460  
 Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val  
 465 470 475 480  
 Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu  
 485 490 495  
 Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr  
 500 505 510  
 Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu  
 515 520 525  
 Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu  
 530 535 540  
 Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His  
 545 550 555 560  
 Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala  
 565 570 575  
 Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val  
 580 585 590  
 Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala  
 595 600 605  
 Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val  
 610 615 620  
 Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu  
 625 630 635 640  
 Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro  
 645 650 655  
 Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn  
 660 665 670  
 Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu  
 675 680 685  
 Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln  
 690 695 700  
 Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly  
 705 710 715 720  
 Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val  
 725 730 735  
 Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg  
 740 745 750  
 Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys  
 755 760 765

Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg  
 770 775 780

Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala  
 785 790 795 800

Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala  
 805 810 815

Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp  
 820 825 830

Trp Leu Ser Ala Lys Gly His His His His His His  
 835 840

<210> 465

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 465

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27

<210> 466

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 466

atcaccccgaggacgtcca ggagaag

27

<210> 467

<211> 2532

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic



<400> 467

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac	180
gggtacaagg ccgtcatcgt ggtctttgac gccgaggccc cctccttccg ccacgaggcc	240
tacgaggcct acaaggcggg gagggccccg acccccagag acttcccccg gcagctcgcc	300
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gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc	420
atcctcaccg ccgaccgcga cctctaccaa ctctgtctccg accgcgtcgc cgtcctccac	480
cccgagggcc acctcatcac ccgaaggac gtccaggaga agtacggggg gccccggag	540
cgctgggtgg acttccgcgc cctcacgggg gaccgctcgg acaacatccc cggggtggcg	600
gggatagggg agaagaccgc ctttcgactc ctgcagagt gggggagcgt ggaaaacctc	660
ctgaagaacc tggaccgggt aaagccggac tcgctccggc gcaagataga ggcgcacctc	720
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 gaccccccta tgcgccgggc ggccaagacg gtgaacttcg gcgtcctcta cgcatgtcc 2040  
 gcccataggc tctcccagga gcttgccatc ccctacgagg aggcgggtggc ctttatagag 2100  
 cgctacttcc aaagcttccc caaggtgcgg gcctggatag aaaagaccct ggaggagggg 2160  
 aggaagcggg gctacgtgga aaccctcttc ggaagaaggc gctacgtgcc cgacctcaac 2220  
 gcccggtga agagcgtcag ggaggccgcg gagcgcatgg cttcaacat gcccggtccag 2280  
 ggcaccgccg ccgacctcat gaagctcgcc atggtgaagc tcttcccccg cctccgggag 2340  
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 cgggcccagg aggtggcggc tttggccaag gaggccatgg agaaggccta tcccctcgcc 2460  
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 caccaccacc ac 2532

<210> 468

<211> 844

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 468

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	

Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
 130 135 140  
 Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
 145 150 155 160  
 Pro Glu Gly His Leu Ile Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly  
 165 170 175  
 Val Pro Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg  
 180 185 190  
 Ser Asp Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu  
 195 200 205  
 Arg Leu Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu  
 210 215 220  
 Asp Arg Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu  
 225 230 235 240  
 Glu Asp Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu  
 245 250 255  
 Pro Leu Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu  
 260 265 270  
 Glu Gly Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu  
 275 280 285  
 His Glu Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro  
 290 295 300  
 Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys  
 305 310 315 320  
 Glu Pro Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly  
 325 330 335  
 Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys  
 340 345 350  
 Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg  
 355 360 365  
 Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr  
 370 375 380  
 Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr  
 385 390 395 400  
 Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu  
 405 410 415  
 Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu  
 420 425 430  
 Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala  
 435 440 445  
 His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala  
 450 455 460

Leu 465	Ser	Leu	Glu	Leu	Ala 470	Glu	Glu	Ile	Arg	Arg 475	Leu	Glu	Glu	Glu	Val 480
Phe	Arg	Leu	Ala	Gly 485	His	Pro	Phe	Asn	Leu 490	Asn	Ser	Arg	Asp	Gln	Leu 495
Glu	Arg	Val	Leu 500	Phe	Asp	Glu	Leu	Arg 505	Leu	Pro	Ala	Leu	Lys 510	Lys	Thr
Lys	Lys	Thr 515	Gly	Lys	Arg	Ser	Thr 520	Ser	Ala	Ala	Val	Leu 525	Glu	Ala	Leu
Arg	Glu 530	Ala	His	Pro	Ile	Val 535	Glu	Lys	Ile	Leu	Gln 540	His	Arg	Glu	Leu
Thr 545	Lys	Leu	Lys	Asn	Thr 550	Tyr	Val	Asp	Pro	Leu 555	Pro	Ser	Leu	Val	His 560
Pro	Arg	Thr	Gly	Arg 565	Leu	His	Thr	Arg	Phe 570	Asn	Gln	Thr	Ala	Thr 575	Ala
Thr	Gly	Arg	Leu 580	Ser	Ser	Ser	Asp	Pro 585	Asn	Leu	Gln	Asn	Ile 590	Pro	Val
Arg	Thr 595	Pro	Leu	Gly	Gln	Arg	Ile 600	Arg	Arg	Ala	Phe	Val 605	Ala	Glu	Ala
Gly 610	Trp	Ala	Leu	Val	Ala	Leu	Asp 615	Tyr	Ser	Gln	Ile 620	Glu	Leu	Arg	Val
Leu 625	Ala	His	Leu	Ser	Gly 630	Asp	Glu	Asn	Leu	Ile 635	Arg	Val	Phe	Gln	Glu 640
Gly	Lys	Asp	Ile	His 645	Thr	Gln	Thr	Ala	Ser 650	Trp	Met	Phe	Gly	Val 655	Pro
Pro	Glu	Ala	Val 660	Asp	Pro	Leu	Met	Arg 665	Arg	Ala	Ala	Lys	Thr 670	Val	Asn
Phe	Gly 675	Val	Leu	Tyr	Gly	Met	Ser 680	Ala	His	Arg	Leu	Ser 685	Gln	Glu	Leu
Ala 690	Ile	Pro	Tyr	Glu	Glu	Ala 695	Val	Ala	Phe	Ile 700	Glu	Arg	Tyr	Phe	Gln
Ser 705	Phe	Pro	Lys	Val	Arg 710	Ala	Trp	Ile	Glu	Lys 715	Thr	Leu	Glu	Glu	Gly 720
Arg	Lys	Arg	Gly	Tyr 725	Val	Glu	Thr	Leu	Phe 730	Gly	Arg	Arg	Arg	Tyr 735	Val
Pro	Asp	Leu	Asn 740	Ala	Arg	Val	Lys	Ser 745	Val	Arg	Glu	Ala	Ala	Glu	Arg
Met	Ala	Phe 755	Asn	Met	Pro	Val	Gln 760	Gly	Thr	Ala	Ala	Asp 765	Leu	Met	Lys
Leu 770	Ala	Met	Val	Lys	Leu	Phe 775	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg
Met 785	Leu	Leu	Gln	Val	Ala 790	Asn	Glu	Leu	Leu	Leu 795	Glu	Ala	Pro	Gln	Ala 800

Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala  
805 810 815  
Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp  
820 825 830  
Trp Leu Ser Ala Lys Gly His His His His His His  
835 840

<210> 469

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 469

ctcgaggcgg gtaaacccca ggaggtc

27

<210> 470

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 470

gggtttaccc gcctcgaggt gcccggc

27

<210> 471

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 471

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60

ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc

120

gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac

180

gggtacaagg ccgtcatcgt ggtctttgac gccgaggccc cctccttcg ccacgaggcc

240

tacgaggcct acaaggcggg gagggccccc acccccagg acttcccccg gcagctcgcc

300

ctcatcaagg agctggtgga cctcctggggg tttacccgcc tcgaggtgcc gggctttgaa	360
gcggatgacg tcctggctac cctggccaag aaggcggaaa aggaaggcta cgaagtgcgc	420
atcctcaccg cggaccggga cctttaccag cttctttcgg agcgaatctc catccttcac	480
ccggagggtt acctgatcac cccggagtgg ctttgggaga agtatgggct taagccttcc	540
cagtgggtgg actaccgggc cttggccggg gacccttcgg acaacatccc cggcgtgaag	600
ggcatcgggg agaagacggc ggccaagctg atccgggagt ggggaagcct ggaaaacctt	660
cttaagcacc tggaacaggt gaaacctgcc tccgtgcggg agaagatcct tagccacatg	720
gaggacctca agctatccct ggagctatcc cgggtgcaca cggacttgct ccttcaggtg	780
gacttcgccc ggcgcgggga gccggaccgg gaggggctta aggccttttt ggagaggctg	840
gagttcggaa gcctcctcca cgagttcggc ctggtgaaa gcccggtggc ggcggaggaa	900
gctccctggc cgcggggcga gggagccttc gtggggtagc ttctttcccg ccccgagccc	960
atgtgggcgg agcttaacgc cttggccgcc gcctggggcg gccgcgtgca ccgggcagca	1020
gaccccttgg cggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc	1080
gccgtcttgg cctcgaggga ggggctagac ctcgtagccg gggacgacct catgctcctc	1140
gcctacctcc tggaccttc gaacaccacc cccgaggggg tggcgcggcg ctacgggggg	1200
gagtggacgg aggacgcgc ccaccgggc ctcctctcgg agaggctcca tcggaacctc	1260
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ctctcccggg tcctggccca tatggaggcc accggggtac ggcgggacgt ggcctacctt	1380
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gagcttaggc ttccgcctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc	1560
gcggtgctgg aggcctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg	1620
gagctcacca agctcaagaa cacctacgtg gacccctcc caagcctcgt ccacccgagg	1680
acgggcccgc tccacaccg cttcaaccag acggccacgg ccacggggag gcttagtagc	1740
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gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc	1860
cgcgtcctcg ccacctctc cggggacgaa aacctgatca gggctttcca ggaggggaag	1920
gacatccaca cccagaccgc aagctggatg ttcggcgctc ccccgagggc cgtggacccc	1980
ctgatgcgcc gggcgggcaa gacggtgaac ttcggcgctc tctacggcat gtccgcccat	2040
aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac	2100
ttcaaagct tcccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag	2160

cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccgcacct caacgcccgg 2220  
 gtgaagagcg tcagggaggc cgcgagcgc atggccttca acatgcccgt ccagggcacc 2280  
 gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340  
 gcccgcatgc tcctccaggt cgccaacgag ctctctctgg agggccccca agcgcgggcc 2400  
 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460  
 ctggaggtgg aggtggggat gggggaggac tggttttccg ccaagggtca ccaccaccac 2520  
 caccac 2526

<210> 472

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 472

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	50	55	60	
Val	Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	65	70	75	80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	85	90	95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	100	105	110	
Arg	Leu	Glu	Val	Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125	
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140	
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	145	150	155	160

Pro Glu Gly Tyr Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
 165 170 175  
 Leu Lys Pro Ser Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro  
 180 185 190  
 Ser Asp Asn Ile Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala  
 195 200 205  
 Lys Leu Ile Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys His Leu  
 210 215 220  
 Glu Gln Val Lys Pro Ala Ser Val Arg Glu Lys Ile Leu Ser His Met  
 225 230 235 240  
 Glu Asp Leu Lys Leu Ser Leu Glu Leu Ser Arg Val His Thr Asp Leu  
 245 250 255  
 Leu Leu Gln Val Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly  
 260 265 270  
 Leu Lys Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro  
 290 295 300  
 Pro Pro Glu Gly Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320  
 Met Trp Ala Glu Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val  
 325 330 335  
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350  
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365  
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460  
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495



Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
500 505 510  
Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
515 520 525  
Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
530 535 540  
Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
545 550 555 560  
Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
565 570 575  
Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
580 585 590  
Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
595 600 605  
Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
610 615 620  
His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
625 630 635 640  
Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
645 650 655  
Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
660 665 670  
Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
675 680 685  
Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
690 695 700  
Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
705 710 715 720  
Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
725 730 735  
Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
740 745 750  
Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
755 760 765  
Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
770 775 780  
Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
820 825 830

Ser Ala Lys Gly His His His His His His  
835 840

<210> 473

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 473

aagccactcc ggggtgatca ggtaacc

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<210> 474

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 474

atcaccccgg agtggctttg ggagaag

27

<210> 475

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 475

atgaattccc tgccccctctt tgagcccaag ggccgggtgc ttctggtgga cggccaccac

60

ctggcctacc gtaccttttt tgccctgaag ggcctcacca ccagccgcgg ggagccggtc

120

caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagggaaga cggggatgtg

180

gtgatcgtgg tctttgacgc cgaggccccc tccttcgcgc accagacctt cgaggcctac

240

aaggcggggc gggctcccac ccccgaggac tttcccgcgc agcttgccct tatcaaggag

300

atggtggacc ttttgggcct ggagcgcctc gaggtgccgg gctttgaagc ggatgacgtc	360
ctggctaccc tggccaagaa ggcggaagaa gaaggctacg aagtgcgcat cctcaccgcg	420
gaccgggacc ttaccagct tctttcggag cgaatctcca tccttcaccc ggaggggttac	480
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aagaccgccc tcaagctcct caaggagtgg ggaagcctgg aaaacctcct caagaacctg	660
gaccgggtaa agccagaaaa cgtccgggag aagatcaagg cccacctgga agacctcagg	720
ctctccttgg agctctcccg ggtgcgcacc gacctcccc tggaggtgga cctcgcccag	780
gggcgggagc ccgaccggga ggggcttagg gccttcctgg agaggctgga gttcggcagc	840
ctcctccacg agttcggcct cctggaggcc cccgcccccc tggaggaggc cccctggccc	900
ccgccggaag gggccttcgt gggcttcgtc ctctcccgcc ccgagcccat gtgggcggag	960
cttaaagccc tggccgcctg caggggcggc cgcgtgcacc gggcagcaga ccccttggcg	1020
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gaggggggtt gggcgttggt ggccctggac tatagccaga tagagctccg cgtcctcgcc	1860
cacctctccg gggacgaaaa cctgatcagg gtcttccagg aggggaagga catccacacc	1920
cagaccgcaa gctggatggt cggcgcccc cggaggccg tggacccct gatgcgccg	1980
gcgccaaga cggatgaactt cggcgctctc tacggcatgt ccgccatag gctctcccag	2040
gagcttgcca tccccacga ggaggcggtg gcctttatag agcgctactt ccaaagcttc	2100
cccaaggtgc gggcctggat agaaaagacc ctggaggagg ggaggaagcg gggctacgtg	2160

gaaaccctct tcggaagaag gcgctacgtg cccgacctca acgcccgggt gaagagcgtc 2220  
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 atgaagctcg ccatggtgaa gctcttcccc cgctccggg agatgggggc ccgcatgctc 2340  
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 gctttggcca aggaggccat ggagaaggcc tatcccctcg ccgtgcccct ggaggtggag 2460  
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<210> 476

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 476

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	1	5	10	15
Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu	20	25	30	
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys	35	40	45	
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val	50	55	60	
Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr	65	70	75	80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala	85	90	95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu	Val	100	105	110	
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala	115	120	125	
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu	130	135	140	
Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly	Tyr	145	150	155	160
Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	Glu	165	170	175	
Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	Ser	Asp	Asn	Leu	180	185	190	

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu Leu Lys  
 195 200 205  
 Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg Val Lys  
 210 215 220  
 Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp Leu Arg  
 225 230 235 240  
 Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu Glu Val  
 245 250 255  
 Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg Ala Phe  
 260 265 270  
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
 275 280 285  
 Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
 290 295 300  
 Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu  
 305 310 315 320  
 Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg Ala Ala  
 325 330 335  
 Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu  
 340 345 350  
 Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val  
 355 360 365  
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380  
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 385 390 395 400  
 Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu  
 405 410 415  
 Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu  
 420 425 430  
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445  
 Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala  
 450 455 460  
 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His  
 465 470 475 480  
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp  
 485 490 495  
 Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg  
 500 505 510  
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
 515 520 525

Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr  
530 535 540  
Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu  
545 550 555 560  
His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
565 570 575  
Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
580 585 590  
Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala  
595 600 605  
Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
610 615 620  
Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr  
625 630 635 640  
Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro  
645 650 655  
Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly  
660 665 670  
Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
675 680 685  
Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg  
690 695 700  
Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val  
705 710 715 720  
Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg  
725 730 735  
Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
740 745 750  
Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu  
755 760 765  
Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala  
770 775 780  
Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala  
785 790 795 800  
Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro  
805 810 815  
Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly  
820 825 830  
His His His His His  
835

<210> 477  
 <211> 64  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic  
 <400> 477  
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 tggc 64  
 <210> 478  
 <211> 64  
 <212> DNA  
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 <220>  
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 <400> 478  
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 ggtg 64  
 <210> 479  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence  
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 caggaagcgg ccgcgtcgac atgaccatga ttacgccaag c 41  
 <210> 480  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence  
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<400> 480  
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<210> 481  
 <211> 3135  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic

<400> 481  
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 gaaccgggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180  
 ggggtacaagg ccgtcttcgt ggtctttgac gccaaagccc cctccttcog ccacgaggcc 240  
 tacgaggcct acaaggcggg gagggccccg acccccgagg acttcccccg gcagctcgcc 300  
 ctcatcaagg agctggtgga cctcctgggg ttaccocgcc tcgaggctcc cggctacgag 360  
 gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420  
 atcctcaccg ccgaccgga cctctacca ctcgtctccg accgctcgc cgtcctccac 480  
 cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540  
 cagtgggtgg acttcgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag 600  
 ggcacgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660  
 ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggccacctg 720  
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 gacctcgccc agggggcggg gcccgaccgg gaggggctta gggccttcct ggagaggctg 840  
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 gcccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc 960  
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 gccgtcttg cctcgaggga ggggctagac ctcgtgccc gggacgacc catgctctc 1140  
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 gagtggacgg aggacgcgc ccaccgggcc ctctctcgg agaggctcca tcggaacctc 1260  
 cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgagg ggaaaagccc 1320  
 ctctcccggt tcctggccca tatggaggcc accggggtac ggcgggacgt ggcctacctt 1380



caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttccgc	1440
ttggcggggcc accccttcaa cctcaactcc cgggaccagc tggaaagggg gctctttgac	1500
gagcttaggc ttcccgctt gaagaagacg aagaagacag gcaagcgctc caccagcgcc	1560
gcggtgctgg aggccctacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg	1620
gagctcacca agctcaagaa cacctacgtg gacccccctcc caagcctcgt ccacccgagg	1680
acgggccgcc tccacaccg cttcaaccag acggccacgg ccacggggag gcttagtagc	1740
tccgaccca acctgcagaa catccccgtc cgcacccccct tgggccagag gatccgccgg	1800
gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc	1860
cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctttcca ggaggggaag	1920
gacatccaca ccagaccgc aagctggatg ttcggcgctc ccccgagggc cgtggacccc	1980
ctgatgcgcc gggcgggcaa gacggtgaac ttcggcgctc tctacggcat gtccgcccac	2040
aggctctccc aggagcttgc catccccctac gaggaggcgg tggcctttat agagcgctac	2100
ttccaaagct tcccaaggt gcgggcctgg atagaaaaga ccctggagga ggggaggaag	2160
cggggctacg tggaaaccct cttcggaaga aggcgtacg tgcccgcact caacgcccgg	2220
gtgaagagcg tcagggaggc cgcggagcgc atggccttca acatgcccggt ccagggcacc	2280
gccgcgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg	2340
gcccgcacgc tcctccaggt cgccaacgag ctctcctcgt agggccccca agcgcggggc	2400
gaggagggtg cggttttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc	2460
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caccacgtcg acatgaccat gattacgcca agctattttag gtgacactat agaatactca	2580
agctatgcat caagcttggt accgagctcg gatccactag taacggccgc cagtgtgctg	2640
gaattctgca gatatccatc aactggcg ggctcgagc atgcatctag agggcccaat	2700
tcgccctata gtgagtcgta ttacaattca ctggccgtcg ttttacaacg tcgtgactgg	2760
gaaaaccctg gcgttaccca acttaatcgc cttgcagcac atcccccttt cgccagctgg	2820
cgtaatagcg aagaggcccg caccgatcgc ccttcccaac agttgcgcag cctgaatggc	2880
gaatgggacg cgccctgtag cggcgcatca agcgcggcgg gtgtgggtgg tacgcgcagc	2940
gtgaccgcta cacttgccag cgccctagcg cccgctcctt tcgctttctt cccttccttt	3000
ctcgccacgt tcgccggctt tccccgtaa gctctaaatc gggggctccc tttagggttc	3060
cgatttagag ctttacggca cctcgaccgc aaaaaacttg atttgggtga tgggtcacgt	3120
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<210> 482

<211> 1045

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 482

Met Asn Ser Glu Ala Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val  
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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30  
Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45  
Phe Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala  
50 55 60  
Val Phe Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala  
65 70 75 80  
Tyr Glu Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro  
85 90 95  
Arg Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr  
100 105 110  
Arg Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu  
115 120 125  
Ala Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala  
130 135 140  
Asp Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His  
145 150 155 160  
Pro Glu Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly  
165 170 175  
Leu Arg Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro  
180 185 190  
Ser Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu  
195 200 205  
Lys Leu Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu  
210 215 220  
Asp Arg Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu  
225 230 235 240  
Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
245 250 255

Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270  
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300  
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320  
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335  
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350  
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365  
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460  
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
 500 505 510  
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540  
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560  
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590

Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605  
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
 805 810 815  
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
 820 825 830  
 Ser Ala Lys Gly His His His His His His Val Asp Met Thr Met Ile  
 835 840 845  
 Thr Pro Ser Tyr Leu Gly Asp Thr Ile Glu Tyr Ser Ser Tyr Ala Ser  
 850 855 860  
 Ser Leu Val Pro Ser Ser Asp Pro Leu Val Thr Ala Ala Ser Val Leu  
 865 870 875 880  
 Glu Phe Cys Arg Tyr Pro Ser His Trp Arg Pro Leu Glu His Ala Ser  
 885 890 895  
 Arg Gly Pro Asn Ser Pro Tyr Ser Glu Ser Tyr Tyr Asn Ser Leu Ala  
 900 905 910  
 Val Val Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu  
 915 920 925

Asn Arg Leu Ala Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Glu  
 930 935 940  
 Glu Ala Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly  
 945 950 955 960  
 Glu Trp Asp Ala Pro Cys Ser Gly Ala Leu Ser Ala Ala Gly Val Val  
 965 970 975  
 Val Thr Arg Ser Val Thr Ala Thr Leu Ala Ser Ala Leu Ala Pro Ala  
 980 985 990  
 Pro Phe Ala Phe Phe Pro Ser Phe Leu Ala Thr Phe Ala Gly Phe Pro  
 995 1000 1005  
 Arg Gln Ala Leu Asn Arg Gly Leu Pro Leu Gly Phe Arg Phe Arg  
 1010 1015 1020  
 Ala Leu Arg His Leu Asp Arg Lys Lys Leu Asp Leu Gly Asp Gly  
 1025 1030 1035  
 Ser Arg Ser Gly Pro Ser Pro  
 1040 1045

<210> 483

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 483

cgggacctcg aggcgcgtga accccaggag gtccac

36

<210> 484

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 484

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60

caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag cgggggggag

120

ccgggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg

180

gacgcggtga tcgtggtctt tgacgccaaag gccccctcct tccgccacga ggcctacggg

240

gggtacaagg cgggcccggc cccacgccg gaggactttc cccggcaact cgcctcctc

300

aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac	360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcacccctc	420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccagag	480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg	540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc	600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag	660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg	720
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gtcctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt	1380
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gaggccctac gggaggccca ccccatcgtg gagaagatcc tccagcaccg ggagctcacc	1620
aagctcaaga acacctacgt ggacccccct ccaagcctcg tccaccgag gacgggcccgc	1680
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aacctgcaga acatccccgt ccgcaccccc ttgggcccaga ggatccgccg ggccttcgtg	1800
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gcccacctct ccggggacga aaacctgatc agggctcttc aggaggggaa ggacatccac	1920
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ttcccgaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac	2160

gtggaaaccc tcttcggaag aaggcgctac gtgcccgacc tcaacgcccc ggtgaagagc 2220  
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gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg 2460  
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<210> 485

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 485

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	1	5	10	15
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	20	25	30	
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	35	40	45	
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	50	55	60	
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	100	105	110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	115	120	125	
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	180	185	190	

Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365  
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430  
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
 450 455 460  
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525



Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn  
 530 535 540  
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His  
 625 630 635 640  
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val  
 785 790 795 800  
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val  
 805 810 815  
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys  
 820 825 830  
 Gly His His His His His His  
 835

<210> 486

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 486

gtggaccttc tgggctttac ccgcctcgag gccccg

36

<210> 487

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 487

cggggcctcg aggcgggtaa agcccagaag gtccac

36

<210> 488

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 488

Met Asn Ser Thr Pro Leu Phe Asp Leu Glu Glu Pro Pro Lys Arg Val  
1 5 10 15

Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Tyr Ala Leu  
20 25 30

Ser Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe  
35 40 45

Ala Arg Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Gln Ala Val Val  
50 55 60

Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu  
65 70 75 80

Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95

Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Phe Thr Arg Leu  
 100 105 110  
 Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Arg Glu Gly Met Glu Val Arg Ile Leu Thr Gly Asp Arg  
 130 135 140  
 Asp Phe Phe Gln Leu Leu Ser Glu Lys Val Ser Val Leu Leu Pro Asp  
 145 150 155 160  
 Gly Thr Leu Val Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly Val Pro  
 165 170 175  
 Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg Ser Asp  
 180 185 190  
 Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu Arg Leu  
 195 200 205  
 Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu Glu Asp  
 225 230 235 240  
 Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu Pro Leu  
 245 250 255  
 Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly  
 260 265 270  
 Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro  
 290 295 300  
 Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro  
 305 310 315 320  
 Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly Arg Val  
 325 330 335  
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350  
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365  
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430

Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460  
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
 500 505 510  
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540  
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560  
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575  
 Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605  
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765

Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
770 775 780

Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
785 790 795 800

Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
805 810 815

Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
820 825 830

Ser Ala Lys Gly His His His His His His  
835 840

<210> 489

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 489

tttaccgcgcc tcgaggtgcc gggc

24

<210> 490

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 490

cggcacctcg aggcgggtaa agcccaaaag gtccac

36

<210> 491

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 491

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	1	5	10	15
Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu	20	25	30	
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys	35	40	45	
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val	50	55	60	
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr	65	70	75	80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala	85	90	95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	Glu	Val	100	105	110	
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala	115	120	125	
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu	130	135	140	
Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly	Tyr	145	150	155	160
Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys	Pro	Ser	165	170	175	
Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn	Ile	180	185	190	
Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	Leu	Ile	Arg	195	200	205	
Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu	Glu	Gln	Val	Lys	210	215	220	
Pro	Ala	Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met	Glu	Asp	Leu	Lys	225	230	235	240
Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	His	Thr	Asp	Leu	Leu	Leu	Gln	Val	245	250	255	
Asp	Phe	Ala	Arg	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Lys	Ala	Phe	260	265	270	
Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu	275	280	285	
Glu	Ser	Pro	Val	Ala	Ala	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	290	295	300	
Ala	Phe	Val	Gly	Tyr	Val	Leu	Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	305	310	315	320

Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala  
 325 330 335  
 Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu  
 340 345 350  
 Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val  
 355 360 365  
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380  
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu  
 385 390 395 400  
 Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu  
 405 410 415  
 Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu  
 420 425 430  
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly  
 435 440 445  
 Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala  
 450 455 460  
 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His  
 465 470 475 480  
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp  
 485 490 495  
 Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg  
 500 505 510  
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
 515 520 525  
 Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr  
 530 535 540  
 Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu  
 545 550 555 560  
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
 565 570 575  
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 580 585 590  
 Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala  
 595 600 605  
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 610 615 620  
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr  
 625 630 635 640  
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro  
 645 650 655

Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly  
                   660                                  665                                  670  
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
                   675                                  680                                  685  
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg  
                   690                                  695                                  700  
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val  
                   705                                  710                                  715                                  720  
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg  
                   725                                  730                                  735  
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
                   740                                  745                                  750  
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu  
                   755                                  760                                  765  
 Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala  
                   770                                  775                                  780  
 Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala  
                   785                                  790                                  795                                  800  
 Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro  
                   805                                  810                                  815  
 Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly  
                   820                                  825                                  830  
 His His His His His His  
                   835

<210> 492

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 492

atcgtggtct ttgacgccga ggccccctcc ttcc

34

<210> 493

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic





Glu Asp Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu  
 245 250 255  
 Pro Leu Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly  
 260 265 270  
 Leu Arg Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro  
 290 295 300  
 Pro Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro  
 305 310 315 320  
 Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val  
 325 330 335  
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
 340 345 350  
 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365  
 Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
 370 375 380  
 Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly  
 385 390 395 400  
 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
 405 410 415  
 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
 420 425 430  
 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
 435 440 445  
 Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser  
 450 455 460  
 Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg  
 465 470 475 480  
 Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg  
 485 490 495  
 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
 500 505 510  
 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
 530 535 540  
 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
 545 550 555 560  
 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
 565 570 575

Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr  
 580 585 590  
 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
 595 600 605  
 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
 610 615 620  
 His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys  
 625 630 635 640  
 Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu  
 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700  
 Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
 705 710 715 720  
 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
 805 810 815  
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
 820 825 830  
 Ser Ala Lys Gly His His His His His His  
 835 840

<210> 495

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 495  
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ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggccgggc cccacgccc gaggaacttc cccggcaact cgccctcatc 300  
aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcacctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggccacat ggacgatctg 720  
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
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cccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggccc 960  
gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agaccccttg 1020  
gcgggggctaa aggacctcaa ggaggtcggg ggcctcctcg ccaaggacct cgccgtcttg 1080  
gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgcctacctc 1140  
ctggaccctt cgaacaccac ccccgagggg gtggcgcggc gctacggggg ggagtggacg 1200  
gaggacgccc cccaccgggc cctcctctcg gagaggctcc atcggaacct ccttaagcgc 1260  
ctcgaggggg aggagaagct cctttggctc taccacgagg tggaaaagcc cctctcccgg 1320  
gtcctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt 1380  
tccttgagc ttgaggagga gatccgccgc ctcgaggagg aggtcttccg cttggcgggc 1440  
cacccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg 1500  
cttcccgcct tgaagaagac gaagaagaca ggcaagcgct ccaccagcgc cgcggtgctg 1560  
gaggccctac gggaggccca cccatcgtg gagaagatcc tccagcaccg ggagctcacc 1620  
aagctcaaga acacctacgt ggacccccct ccaagcctcg tccaccgag gacgggcccgc 1680  
ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc 1740  
aacctgcaga acatccccgt ccgcacccc ttgggcccaga ggatccgccg ggccttcgtg 1800  
gccgaggcgg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc 1860

gccacctct ccggggacga aaacctgatc aggggtcttcc aggaggggaa ggacatccac 1920  
 acccagaccg caagctggat gttcggcgtc cccccggagg ccgtggaccc cctgatgcgc 1980  
 cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcca taggctctcc 2040  
 caggagcttg ccatccccta cgaggaggcg gtggccttta tagagcgcta cttccaaagc 2100  
 ttccccaagg tgcgggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160  
 gtggaaaccc tcttcggaag aaggcgctac gtgcccagacc tcaacgcccg ggtgaagagc 2220  
 gtcagggagg ccgcgagcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280  
 ctcatgaagc tcgccatggt gaagctcttc ccccgccctcc gggagatggg ggcccgcgac 2340  
 ctctccagg tcgccaacga gctcctcctg gaggcccccc aagcgcgggc cgaggagggtg 2400  
 gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggagggtg 2460  
 gaggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac 2517

<210> 496

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 496

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70				75					80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365  
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
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 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
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 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
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 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
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 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480

His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys  
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 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn  
 530 535 540  
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
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 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His  
 625 630 635 640  
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr  
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 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala  
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 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val  
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 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val  
 785 790 795 800  
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val  
 805 810 815

Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys  
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Gly His His His His His His  
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<210> 497

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 497

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<210> 498

<211> 842

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 498

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			20					25					30		

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 Ala Arg Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Gln Ala Val Val  
 50 55 60  
 Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Glu  
 65 70 75 80  
 Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
 85 90 95  
 Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg Leu  
 100 105 110  
 Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Arg Glu Gly Met Glu Val Arg Ile Leu Thr Gly Asp Arg  
 130 135 140  
 Asp Phe Phe Gln Leu Leu Ser Glu Lys Val Ser Val Leu Leu Pro Asp  
 145 150 155 160  
 Gly Thr Leu Val Thr Pro Lys Asp Val Gln Glu Lys Tyr Gly Val Pro  
 165 170 175  
 Pro Glu Arg Trp Val Asp Phe Arg Ala Leu Thr Gly Asp Arg Ser Asp  
 180 185 190  
 Asn Ile Pro Gly Val Ala Gly Ile Gly Glu Lys Thr Ala Leu Arg Leu  
 195 200 205  
 Leu Ala Glu Trp Gly Ser Val Glu Asn Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Val Lys Pro Asp Ser Leu Arg Arg Lys Ile Glu Ala His Leu Glu Asp  
 225 230 235 240  
 Leu His Leu Ser Leu Asp Leu Ala Arg Ile Arg Thr Asp Leu Pro Leu  
 245 250 255  
 Glu Val Asp Phe Lys Ala Leu Arg Arg Arg Thr Pro Asp Leu Glu Gly  
 260 265 270  
 Leu Arg Ala Phe Leu Glu Glu Leu Glu Phe Gly Ser Leu Leu His Glu  
 275 280 285  
 Phe Gly Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro  
 290 295 300  
 Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu Ser Arg Lys Glu Pro  
 305 310 315 320  
 Met Trp Ala Glu Leu Leu Ala Leu Ala Ala Ala Ser Gly Gly Arg Val  
 325 330 335  
 His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val  
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 Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly  
 355 360 365

Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu  
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 Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu  
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 His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp  
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 Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met  
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 Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys  
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 Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu  
 515 520 525  
 Ala His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys  
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 Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg  
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 Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly  
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 Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp  
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 Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala  
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 645 650 655  
 Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly  
 660 665 670  
 Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile  
 675 680 685  
 Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe  
 690 695 700

Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys  
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 Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp  
 725 730 735  
 Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala  
 740 745 750  
 Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala  
 755 760 765  
 Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu  
 770 775 780  
 Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala  
 785 790 795 800  
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro  
 805 810 815  
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu  
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 Ser Ala Lys Gly His His His His His His  
 835 840

<210> 499

<211> 2514

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 499

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<210> 500

<211> 838

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 500

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			20					25					30		
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
			35				40					45			
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val
	50					55					60				
Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr
65					70					75					80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
				85					90					95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu	Val
			100					105					110		
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala
		115					120					125			
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg	Asp	Leu
	130					135					140				
Tyr	Gln	Leu	Leu	Ser	Glu	Arg	Ile	Ser	Ile	Leu	His	Pro	Glu	Gly	Tyr
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Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Lys	Pro	Ser
				165					170					175	
Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	Asp	Asn	Ile
			180					185					190		
Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	Leu	Ile	Arg
		195					200					205			
Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	His	Leu	Glu	Gln	Val	Lys
	210					215					220				
Pro	Ala	Ser	Val	Arg	Glu	Lys	Ile	Leu	Ser	His	Met	Glu	Asp	Leu	Lys
225					230					235					240
Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	His	Thr	Asp	Leu	Leu	Leu	Gln	Val
				245					250					255	

Asp Phe Ala Arg Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe  
 260 265 270  
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu  
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 Glu Ser Pro Val Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly  
 290 295 300  
 Ala Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu  
 305 310 315 320  
 Leu Asn Ala Leu Ala Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala  
 325 330 335  
 Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu  
 340 345 350  
 Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val  
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 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn  
 370 375 380  
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 385 390 395 400  
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 405 410 415  
 Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu  
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 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly  
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 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His  
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 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp  
 485 490 495  
 Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg  
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 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile  
 515 520 525  
 Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr  
 530 535 540  
 Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu  
 545 550 555 560  
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser  
 565 570 575  
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln  
 580 585 590

Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala  
 595 600 605  
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly  
 610 615 620  
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr  
 625 630 635 640  
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro  
 645 650 655  
 Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly  
 660 665 670  
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu  
 675 680 685  
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg  
 690 695 700  
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val  
 705 710 715 720  
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg  
 725 730 735  
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro  
 740 745 750  
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu  
 755 760 765  
 Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala  
 770 775 780  
 Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala  
 785 790 795 800  
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<210> 501

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic



<400> 501

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gggtacaagg cgggccgggc cccacgccc gaggactttc cccggcaact cgcctcatc	300
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<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 502

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			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70				75					80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85				90						95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys
	130					135					140				

Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
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 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
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 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
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 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
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 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
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 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415  
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 420 425 430  
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
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 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
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 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
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His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
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 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
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 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
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 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val  
 785 790 795 800

Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala	Val	
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Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	
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			835													

  

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<210> 506

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 506

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
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Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	50	55	60	
Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	65	70	75	80
Gly	Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	85	90	95	
Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	100	105	110	
Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	115	120	125	
Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	130	135	140	
Lys	Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	145	150	155	160
Glu	Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	165	170	175	
Arg	Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	180	185	190	

Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys  
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 Leu Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp  
 210 215 220  
 Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp  
 225 230 235 240  
 Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu  
 245 250 255  
 Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg  
 260 265 270  
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly  
 275 280 285  
 Leu Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro  
 290 295 300  
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp  
 305 310 315 320  
 Ala Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg  
 325 330 335  
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 340 345 350  
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 355 360 365  
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro  
 370 375 380  
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp  
 385 390 395 400  
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg  
 405 410 415  
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr  
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 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
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 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu  
 450 455 460  
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 465 470 475 480  
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
 485 490 495  
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly  
 500 505 510  
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His  
 515 520 525



Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys  
 530 535 540  
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly  
 545 550 555 560  
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
 565 570 575  
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu  
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 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu  
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 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
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 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile  
 625 630 635 640  
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val  
 645 650 655  
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
 660 665 670  
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr  
 675 680 685  
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
 690 695 700  
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly  
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 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn  
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 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val  
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 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln  
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 Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu  
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cgggcggcca	agacggtgaa	cttcggcgtc	ctctacggca	tgtccgcca	taggtctctc	2040
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ttccccaagg	tgcgggcctg	gatagaaaag	accctggagg	aggggaggaa	gcggggctac	2160
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<210> 510

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 510

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	1	5	10	15
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	20	25	30	
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	35	40	45	
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	50	55	60	
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	100	105	110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	115	120	125	
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	180	185	190	
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	195	200	205	
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	210	215	220	

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365  
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430  
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
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 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
 450 455 460  
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys  
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 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
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 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn  
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 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
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 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
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 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr  
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 675 680 685  
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
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 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
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 Gly His His His His His His  
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 ccggtgcagg cgggtctacgg ctccgccaag agcctcctca aggccctcag agaggacggg 180  
 gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggccctacggg 240  
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<210> 514

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 514

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	1	5	10	15
Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	20	25	30	
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	35	40	45	
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Ala	Val	Ile	50	55	60	
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	100	105	110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	115	120	125	
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175	
Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	180	185	190	
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	195	200	205	
Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	210	215	220	

Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365  
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430  
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
 450 455 460  
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn  
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 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
 545 550 555 560

Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His  
 625 630 635 640  
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr  
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 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val  
 785 790 795 800  
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val  
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 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys  
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 Gly His His His His His His  
 835

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<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

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<212> DNA

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<220>

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<210> 518

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 518

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			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70					75					80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys
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Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
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Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp
		180						185					190		
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		195					200					205			
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	210					215					220				
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu
225					230					235					240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu
				245					250					255	



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 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr  
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 ccggtgcagg cgggtctacgg ctccgccaa agcctcctca aggccctcaa ggaggacggg 180  
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<212>	PRT					

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 522

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Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	
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Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	
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Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	
				85					90					95		
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	
			100					105					110			
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	
		115					120					125				
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	
	130					135					140					
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	
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Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	
			180					185					190			
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys	Leu	
		195					200					205				
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	210					215					220					
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Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	Ala	
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 325 330 335  
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
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 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
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 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
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Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His  
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 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr  
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 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
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<400> 523

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Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	50	55	60	
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	100	105	110	
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Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
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Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	210	215	220	
Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	225	230	235	240
Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	245	250	255	
Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Lys	Ala	260	265	270	
Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	275	280	285	
Leu	Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	290	295	300	
Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	305	310	315	320



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 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365  
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430  
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445  
 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
 450 455 460  
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
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 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
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 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys  
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 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn  
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 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His  
 625 630 635 640  
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655

Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr  
                   660                                  665                                  670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
                   675                                  680                                  685  
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
                   690                                  695                                  700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr  
                   705                                  710                                  715                                  720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala  
                                   725                                  730                                  735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
                                   740                                  745                                  750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
                                   755                                  760                                  765  
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val  
                   770                                  775                                  780  
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val  
                   785                                  790                                  795                                  800  
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val  
                                   805                                  810                                  815  
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys  
                                   820                                  825                                  830  
 Gly His His His His His His  
                   835

<210> 527

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 527

gagcccgacc gggaggggct taaggccttt ctggagagg

39

<210> 528

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 528  
cctctccaga aaggccttaa gcccctcccc gtcgggctc 39

<210> 529

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 529  
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caccacctgg cctaccgcac ctccacgcc ctgaagggcc tcaccaccag ccgggggggag 120  
ccggtgcagg cgggtctacgg ctccgccaaag agcctcctca aggccctcaa ggaggacggg 180  
gacgcggtga tcgtggtctt tgacgccgag gccccctcct tccgccacga ggcctacggg 240  
gggtacaagg cgggcccggc cccacgccg gaggactttc cccggcaact cgcctcatc 300  
aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac 360  
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420  
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480  
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540  
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcatc 600  
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660  
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggccacat ggacgatctg 720  
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780  
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840  
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gatcttctgg ccctggccgc cgccaggggc ggccgcgtgc accgggcagc agacccttg 1020  
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tccctggagc ttgcggagga gatccgccgc ctcgaggagg aggtcttccg cttggcgggc 1440  
 cacccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg 1500  
 cttcccgct tgaagaagac gaagaagaca ggcaagcgct ccaccagcgc cgcggtgctg 1560  
 gaggccctac gggaggccca ccccatcgtg gagaagatcc tccagcaccg ggagctcacc 1620  
 aagctcaaga acacctacgt ggacccccctc ccaagcctcg tccacccgag gacgggcccgc 1680  
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 aacctgcaga acatccccgt ccgcaccccc ttgggccaga ggatccgccg ggcttctgtg 1800  
 gccgaggcgg gttgggcgtt ggtggccctg gactatagcc agatagagct ccgcgtcctc 1860  
 gccacacctc ccggggacga aaacctgatc agggcttcc aggaggggaa ggacatccac 1920  
 acccagaccg caagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc 1980  
 cgggcggcca agacggtgaa cttcggcgtc ctctacggca tgtccgcccc taggctctcc 2040  
 caggagcttg ccatccccca cgaggaggcg gtggccttta tagagcgcta cttccaaagc 2100  
 ttcccaagg tgccggcctg gatagaaaag accctggagg aggggaggaa gcggggctac 2160  
 gtggaaaccc tcttcggaag aaggcgctac gtgcccgaac tcaacgcccg ggtgaagagc 2220  
 gtcagggagg ccgcggagcg catggccttc aacatgcccg tccagggcac cgcgccgac 2280  
 ctcatgaagc tcgccatggt gaagctcttc cccgcctcc gggagatggg ggcccgcacg 2340  
 ctctccagg tcgccaacga gctcctcctg gaggccccc aagcgcgggc cgaggaggtg 2400  
 gcggctttgg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggaggtg 2460  
 gaggtgggga tgggggagga ctggctttcc gccaaagggtc accaccacca ccaccac 2517

<210> 530

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 530

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile  
50 55 60  
Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr Gly  
65 70 75 80  
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln  
85 90 95  
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu  
100 105 110  
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
115 120 125  
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
130 135 140  
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
145 150 155 160  
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
165 170 175  
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
180 185 190  
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
195 200 205  
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
210 215 220  
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
225 230 235 240  
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
245 250 255  
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
260 265 270  
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
275 280 285  
Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro Glu  
290 295 300  
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
305 310 315 320  
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
325 330 335  
Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
340 345 350  
Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
355 360 365  
Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
370 375 380

Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	385	390	395	400
Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	His	Arg	Asn	405	410	415	
Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp	Leu	Tyr	His	420	425	430	
Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	Glu	Ala	Thr	435	440	445	
Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser	Leu	Glu	Leu	450	455	460	
Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg	Leu	Ala	Gly	465	470	475	480
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	485	490	495	
Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Lys	Lys	Thr	Lys	Lys	Thr	Gly	Lys	500	505	510	
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	515	520	525	
Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Asn	530	535	540	
Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	Thr	Gly	Arg	545	550	555	560
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	565	570	575	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	580	585	590	
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	Ala	Leu	Val	595	600	605	
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	610	615	620	
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	Asp	Ile	His	625	630	635	640
Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	Ala	Val	Asp	645	650	655	
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr	660	665	670	
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	675	680	685	
Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	690	695	700	
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr	705	710	715	720

Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala  
                     725                                    730                                    735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
                     740                                    745                                    750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
                     755                                    760                                    765  
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val  
                     770                                    775                                    780  
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val  
                     785                                    790                                    795                                    800  
 Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val  
                     805                                    810                                    815  
 Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys  
                     820                                    825                                    830  
 Gly His His His His His His  
                     835

<210> 531

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 531  
 cacgagttcg gccttctggg aggggagaag ccccgggagg aggccccctg gccc

54

<210> 532

<211> 54

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 532  
 gggccagggg gcctcctccc ggggcttctc ccctcccaga aggccgaact cgtg

54

<210> 533

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 533

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ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg	180
gacgcggtga tcgtggtcct tgacgcagag gccccctcct tccgccacga ggcctacggg	240
gggtacaagg cgggcccggc cccacgccg gaggactttc cccggcaact cgcctcctc	300
aaggagctgg tggacctcct ggggttcacg cgcctcgagg tcccgggcta cgaggcggac	360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc	420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag	480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg	540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcctc	600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag	660
aacctggacc ggctgaagcc cggcatccgg gagaagatcc tggcccatat ggacgatctg	720
aagctctcct gggacctggc caagggtgcgc accgacctgc ccctggagggt ggacttcgcc	780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc	840
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gatcttcttg ccctggccgc ctgcaggggc ggccgcgtgc accgggcagc agacccttg	1020
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gcctcgaggg aggggctaga cctcgtgccc ggggacgacc ccatgctcct cgcctacctc	1140
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gtcctggccc atatggaggc caccggggta cggcgggacg tggcctacct tcaggccctt	1380
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cacccttca acctcaactc ccgggaccag ctggaaaggg tgctctttga cgagcttagg	1500
cttcccgcct tgaagaagac gaagaagaca ggcaagcgct ccaccagcgc cgcggtgctg	1560
gaggccctac gggaggccca ccccatcgtg gagaagatcc tccagcaccg ggagctcacc	1620
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ctccacaccc gcttcaacca gacggccacg gccacgggga ggcttagtag ctccgacccc 1740  
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gcggcttttg ccaaggaggc catggagaag gcctatcccc tcgccgtgcc cctggagggtg 2460  
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<210> 534

<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 534

Met	Asn	Ser	Gly	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu
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Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys
			20					25					30		
Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe
		35					40					45			
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile
	50					55					60				
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly
65					70					75				80	
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105						110	

Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys  
 115 120 125  
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys  
 130 135 140  
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu  
 145 150 155 160  
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg  
 165 170 175  
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg Ala  
 325 330 335  
 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
 340 345 350  
 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365  
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430  
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
 435 440 445

Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
 450 455 460  
 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
 485 490 495  
 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys  
 500 505 510  
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
 515 520 525  
 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn  
 530 535 540  
 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
 545 550 555 560  
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser  
 565 570 575  
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly  
 580 585 590  
 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val  
 595 600 605  
 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
 610 615 620  
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His  
 625 630 635 640  
 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr  
 660 665 670  
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr  
 705 710 715 720  
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala  
 725 730 735  
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780

Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val  
785 790 795 800

Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val  
805 810 815

Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys  
820 825 830

Gly His His His His His His  
835

<210> 535

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 535  
ctggccctgg ccgcctgcag gggcggccgc gtg

33

<210> 536

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 536  
cacgcggccg cccctgcagg cggccagggc cag

33

<210> 537

<211> 2517

<212> DNA

<213> Artificial Sequence

<220>

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120

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180

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240

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cgggcggcca	agacggtgaa	cttcggcgtc	ctctacggca	tgtccgcca	taggctctcc	2040
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<211> 839

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 538

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Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	35	40	45	
Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	50	55	60	
Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	65	70	75	80
Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	85	90	95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	100	105	110	
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	Lys	115	120	125	
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	130	135	140	
Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	145	150	155	160
Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	165	170	175	

Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp  
 180 185 190  
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu  
 195 200 205  
 Leu Lys Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg  
 210 215 220  
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu  
 225 230 235 240  
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu  
 245 250 255  
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala  
 260 265 270  
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu  
 275 280 285  
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Glu  
 290 295 300  
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala  
 305 310 315 320  
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala  
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 Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu  
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 Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu  
 355 360 365  
 Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser  
 370 375 380  
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr  
 385 390 395 400  
 Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn  
 405 410 415  
 Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His  
 420 425 430  
 Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr  
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 Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu  
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 Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly  
 465 470 475 480  
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe  
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 Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys  
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Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro  
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 Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn  
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 Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg  
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 565 570 575  
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 Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val  
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 Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser  
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 Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp  
 645 650 655  
 Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr  
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 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu  
 675 680 685  
 Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val  
 690 695 700  
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr  
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 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala  
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 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met  
 740 745 750  
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys  
 755 760 765  
 Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val  
 770 775 780  
 Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val  
 785 790 795 800  
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 Gly His His His His His His  
 835



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<210> 542

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 542

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	1	5	10	15
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	20	25	30	
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	35	40	45	
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Ala	Val	50	55	60	
Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	65	70	75	80
Gly	Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	85	90	95	
Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	100	105	110	
Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	115	120	125	
Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	130	135	140	
Lys	Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	145	150	155	160
Glu	Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	165	170	175	
Arg	Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	180	185	190	
Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys	195	200	205	
Leu	Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	210	215	220	

Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp  
 225 230 235 240  
 Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu  
 245 250 255  
 Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys  
 260 265 270  
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly  
 275 280 285  
 Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro  
 290 295 300  
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp  
 305 310 315 320  
 Ala Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg  
 325 330 335  
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly  
 340 345 350  
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp  
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 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro  
 370 375 380  
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp  
 385 390 395 400  
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg  
 405 410 415  
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr  
 420 425 430  
 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
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 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu  
 450 455 460  
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala  
 465 470 475 480  
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
 485 490 495  
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly  
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 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His  
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 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys  
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 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly  
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Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
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 595 600 605  
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
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 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile  
 625 630 635 640  
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val  
 645 650 655  
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
 660 665 670  
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr  
 675 680 685  
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
 690 695 700  
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly  
 705 710 715 720  
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn  
 725 730 735  
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
 740 745 750  
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val  
 755 760 765  
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln  
 770 775 780  
 Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu  
 785 790 795 800  
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala  
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<210> 543

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

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<210> 544

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 544

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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Ala	Val
	50					55					60				
Ile	Val	Val	Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr
65					70					75				80	
Gly	Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg
			85						90					95	

Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg  
 100 105 110  
 Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala  
 115 120 125  
 Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp  
 130 135 140  
 Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro  
 145 150 155 160  
 Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu  
 165 170 175  
 Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser  
 180 185 190  
 Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys  
 195 200 205  
 Leu Leu Lys Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp  
 210 215 220  
 Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp  
 225 230 235 240  
 Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu  
 245 250 255  
 Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys  
 260 265 270  
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly  
 275 280 285  
 Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro  
 290 295 300  
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp  
 305 310 315 320  
 Ala Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg  
 325 330 335  
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly  
 340 345 350  
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp  
 355 360 365  
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro  
 370 375 380  
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp  
 385 390 395 400  
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg  
 405 410 415  
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr  
 420 425 430



His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
 435 440 445  
 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu  
 450 455 460  
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala  
 465 470 475 480  
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
 485 490 495  
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly  
 500 505 510  
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His  
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 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys  
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 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu  
 595 600 605  
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
 610 615 620  
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile  
 625 630 635 640  
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val  
 645 650 655  
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
 660 665 670  
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr  
 675 680 685  
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
 690 695 700  
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly  
 705 710 715 720  
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn  
 725 730 735  
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
 740 745 750  
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val  
 755 760 765

Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln  
 770 775 780

Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu  
 785 790 795 800

Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala  
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Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala  
 820 825 830

Lys Gly His His His His His His  
 835 840

<210> 545

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 545

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50

<210> 546

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 546

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50

<210> 547

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 547

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33

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 cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga 180  
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<210> 550

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 550

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			20					25					30			
Tyr	Gln	Phe	Ile	Ser	Ile	Ile	Arg	Gln	Pro	Asp	Gly	Thr	Pro	Leu	Lys	
		35					40					45				
Asp	Ser	Gln	Gly	Arg	Ile	Thr	Ser	His	Leu	Ser	Gly	Ile	Leu	Tyr	Arg	
	50					55					60					
Val	Ser	Asn	Met	Val	Glu	Val	Gly	Ile	Arg	Pro	Val	Phe	Val	Phe	Asp	
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Gly	Glu	Pro	Pro	Glu	Phe	Lys	Lys	Ala	Glu	Ile	Glu	Glu	Arg	Lys	Lys	
				85					90					95		
Arg	Arg	Ala	Glu	Ala	Glu	Glu	Met	Trp	Ile	Ala	Ala	Leu	Gln	Ala	Gly	
			100					105					110			
Asp	Lys	Asp	Ala	Lys	Lys	Tyr	Ala	Gln	Ala	Ala	Gly	Arg	Val	Asp	Glu	
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Tyr	Ile	Val	Asp	Ser	Ala	Lys	Thr	Leu	Leu	Ser	Tyr	Met	Gly	Ile	Pro	
	130					135					140					
Phe	Val	Asp	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ala	Tyr	Met	Ala	
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Ala	Lys	Gly	Asp	Val	Glu	Tyr	Thr	Gly	Ser	Gln	Asp	Tyr	Asp	Ser	Leu	
				165					170					175		
Leu	Phe	Gly	Ser	Pro	Arg	Leu	Ala	Arg	Asn	Leu	Ala	Ile	Thr	Gly	Lys	
			180					185					190			
Arg	Lys	Leu	Pro	Gly	Lys	Asn	Val	Tyr	Val	Asp	Val	Lys	Pro	Glu	Ile	
		195					200					205				
Ile	Ile	Leu	Glu	Ser	Asn	Leu	Lys	Arg	Leu	Gly	Leu	Thr	Arg	Glu	Gln	
	210					215					220					
Leu	Ile	Asp	Ile	Ala	Ile	Leu	Val	Gly	Thr	Asp	Ala	Asn	Glu	Gly	Val	
225					230					235					240	
Lys	Gly	Val	Gly	Val	Lys	Lys	Ala	Leu	Asn	Tyr	Ile	Lys	Thr	Tyr	Gly	
				245					250					255		

Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val  
 260 265 270  
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr  
 275 280 285  
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu  
 290 295 300  
 Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu  
 305 310 315 320  
 Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe  
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<210> 551

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 551

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33

<210> 552

<211> 1008

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 552

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cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga	180
atcctataca gagtctccaa catgggtcgag gtgggaatca ggccggtgtt tgtattcgac	240
ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggtgag	300
gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct	360
caggctgcag ggaggggttga cgagtacatt gttgactccg caaagacgct ttttaagttac	420
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gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcgggaagc	540
ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaaatgtc	600

tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctggggtttg 660  
acgaggggagc agctcatcga catagcgatt ctggtcggga cggacaggaa tgaggggtgtg 720  
aaggggtgtcg gcgtcaagaa ggctttgaac tacatcaaga cctacggaga tatttttcagg 780  
gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttcctg 840  
aatcctcctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc 900  
atcgagttcc tgtgcgagga gcacgacttc agcaggggaga gggtcgagaa ggccttggag 960  
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<210> 553

<211> 336

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 553

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Tyr	Gln	Phe	Ile	Ser	Ile	Ile	Arg	Gln	Pro	Asp	Gly	Thr	Pro	Leu	Lys	35	40	45	
Asp	Ser	Gln	Gly	Arg	Ile	Thr	Ser	His	Leu	Ser	Gly	Ile	Leu	Tyr	Arg	50	55	60	
Val	Ser	Asn	Met	Val	Glu	Val	Gly	Ile	Arg	Pro	Val	Phe	Val	Phe	Asp	65	70	75	80
Gly	Glu	Pro	Pro	Glu	Phe	Lys	Lys	Ala	Glu	Ile	Glu	Glu	Arg	Lys	Lys	85	90	95	
Arg	Arg	Ala	Glu	Ala	Glu	Glu	Met	Trp	Ile	Ala	Ala	Leu	Gln	Ala	Gly	100	105	110	
Asp	Lys	Asp	Ala	Lys	Lys	Tyr	Ala	Gln	Ala	Ala	Gly	Arg	Val	Asp	Glu	115	120	125	
Tyr	Ile	Val	Asp	Ser	Ala	Lys	Thr	Leu	Leu	Ser	Tyr	Met	Gly	Ile	Pro	130	135	140	
Phe	Val	Asp	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ala	Tyr	Met	Ala	145	150	155	160

Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu  
 165 170 175  
 Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys  
 180 185 190  
 Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile  
 195 200 205  
 Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln  
 210 215 220  
 Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Arg Asn Glu Gly Val  
 225 230 235 240  
 Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly  
 245 250 255  
 Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val  
 260 265 270  
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr  
 275 280 285  
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu  
 290 295 300  
 Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu  
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 Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe  
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<210> 554

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 554

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20

<210> 555

<211> 36

<212> DNA

<213> Artificial Sequence

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<223> Synthetic

<400> 555

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36

<210> 556

<211> 1011

<212> DNA

<213> Archaeoglobus fulgidus

<400> 556

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atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggtcgagaa ggcccttgag	960
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<210> 557

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 557

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<210> 558

<211> 2526

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 558

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<211> 2643

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

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<211> 881

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 560

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Tyr	Gln	Phe	Ile	Ser	Ile	Ile	Arg	Gln	Pro	Asp	Gly	Thr	Pro	Leu	Lys	35	40	45	
Asp	Ser	Gln	Gly	Arg	Ile	Thr	Ser	His	Leu	Ser	Gly	Ile	Leu	Tyr	Arg	50	55	60	
Val	Ser	Asn	Met	Val	Glu	Val	Gly	Ile	Arg	Pro	Val	Phe	Val	Phe	Asp	65	70	75	80
Gly	Glu	Pro	Pro	Glu	Phe	Lys	Lys	Ala	Glu	Ile	Glu	Glu	Arg	Lys	Lys	85	90	95	
Arg	Arg	Ala	Glu	Ala	Glu	Glu	Met	Trp	Ile	Ala	Ala	Leu	Gln	Ala	Gly	100	105	110	
Asp	Lys	Asp	Ala	Lys	Lys	Tyr	Ala	Gln	Ala	Ala	Gly	Arg	Val	Asp	Glu	115	120	125	
Tyr	Ile	Val	Asp	Ser	Ala	Lys	Thr	Leu	Leu	Ser	Tyr	Met	Gly	Ile	Pro	130	135	140	
Phe	Val	Asp	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ala	Tyr	Met	Ala	145	150	155	160
Ala	Lys	Gly	Asp	Val	Glu	Tyr	Thr	Gly	Ser	Gln	Asp	Tyr	Asp	Ser	Leu	165	170	175	

Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys  
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 Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile  
 195 200 205  
 Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln  
 210 215 220  
 Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val  
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 Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly  
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 Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu  
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 325 330 335  
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 Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala  
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 Ala Cys Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly  
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 Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro  
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 595 600 605  
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 645 650 655  
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 660 665 670  
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 675 680 685  
 Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala  
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 740 745 750  
 Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly  
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 770 775 780  
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 785 790 795 800  
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 Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu  
 820 825 830  
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Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val  
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<210> 561

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 561

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21

<210> 562

<211> 36

<212> DNA

<213> Artificial Sequence

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<400> 562

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36

<210> 563

<211> 2619

<212> DNA

<213> Artificial Sequence

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<400> 563

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120

cagcctgaag gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga

180

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<211> 873

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 564

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Tyr	Gln	Phe	Ile	Ser	Ile	Ile	Arg	Gln	Pro	Asp	Gly	Thr	Pro	Leu	Lys	35	40	45	
Asp	Ser	Gln	Gly	Arg	Ile	Thr	Ser	His	Leu	Ser	Gly	Ile	Leu	Tyr	Arg	50	55	60	
Val	Ser	Asn	Met	Val	Glu	Val	Gly	Ile	Arg	Pro	Val	Phe	Val	Phe	Asp	65	70	75	80
Gly	Glu	Pro	Pro	Glu	Phe	Lys	Lys	Ala	Glu	Ile	Glu	Glu	Arg	Lys	Lys	85	90	95	
Arg	Arg	Ala	Glu	Ala	Glu	Glu	Met	Trp	Ile	Ala	Ala	Leu	Gln	Ala	Gly	100	105	110	
Asp	Lys	Asp	Ala	Lys	Lys	Tyr	Ala	Gln	Ala	Ala	Gly	Arg	Val	Asp	Glu	115	120	125	
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Phe	Val	Asp	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ala	Tyr	Met	Ala	145	150	155	160
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 Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln  
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 Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val  
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 Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly  
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 260 265 270  
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 275 280 285  
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu  
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 Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu  
 305 310 315 320  
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 Pro Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met  
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 Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His  
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 Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg  
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 Pro Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu  
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Ala Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val  
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Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr  
530 535 540  
Gly Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala  
545 550 555 560  
His Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu  
565 570 575  
Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr  
580 585 590  
Gly Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg  
595 600 605  
Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro  
610 615 620  
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625 630 635 640  
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645 650 655  
Leu Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp  
660 665 670  
Ile His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala  
675 680 685  
Val Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val  
690 695 700  
Leu Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro  
705 710 715 720  
Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro  
725 730 735  
Lys Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg  
740 745 750  
Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu  
755 760 765  
Asn Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe  
770 775 780  
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785 790 795 800  
Val Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu  
805 810 815  
Gln Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu  
820 825 830  
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<212> DNA

<213> Artificial Sequence

<220>

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<400> 565

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<210> 566

<211> 881

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 566

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Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
35     40     45
Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
50     55     60
Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
65     70     75     80
Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
85     90     95
Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
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Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
115    120   125
Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
130    135   140
Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
145    150   155   160
Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
165    170   175
Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
180    185   190
Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
195    200   205
Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
210    215   220
Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
225    230   235   240
Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
245    250   255
Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
260    265   270
Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
275    280   285
Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
290    295   300
Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
305    310   315   320

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Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe  
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 Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala  
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 Ala Cys Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala  
 370 375 380  
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 385 390 395 400  
 Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro  
 405 410 415  
 Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly  
 420 425 430  
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 435 440 445  
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 Ala Ile Lys Lys Thr Gln Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala  
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 565 570 575  
 Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr Tyr Ile Asp Pro Leu  
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 Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn  
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 625 630 635 640  
 Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala Leu Asp Tyr Ser Gln  
 645 650 655

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Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala
	690					695					700				
Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg
705				710						715					720
Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu	Ala	Gln	Ala	Phe	Ile
			725						730					735	
Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys
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Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly
	755						760					765			
Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	Arg	Val	Lys	Ser	Val	Arg
	770					775					780				
Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala
785					790					795					800
Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Glu
			805						810					815	
Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	Ala	Asn	Glu	Leu	Val	Leu
			820					825					830		
Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	Ala	Arg	Leu	Ala	Lys	Glu
		835					840					845			
Val	Met	Glu	Gly	Val	Tyr	Pro	Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val
	850					855					860				
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His

<210> 567

<211> 2643

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic



<400> 567

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gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct	360
caggctgcag ggaggggttga cgagtacatt gttgactccg caaagacgct ttttaagttac	420
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gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcgggaagc	540
ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttccccg caaaaatgtc	600
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<211> 881

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 568

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			20					25					30		
Tyr	Gln	Phe	Ile	Ser	Ile	Ile	Arg	Gln	Pro	Asp	Gly	Thr	Pro	Leu	Lys
		35					40					45			
Asp	Ser	Gln	Gly	Arg	Ile	Thr	Ser	His	Leu	Ser	Gly	Ile	Leu	Tyr	Arg
	50					55					60				
Val	Ser	Asn	Met	Val	Glu	Val	Gly	Ile	Arg	Pro	Val	Phe	Val	Phe	Asp
65					70				75					80	
Gly	Glu	Pro	Pro	Glu	Phe	Lys	Lys	Ala	Glu	Ile	Glu	Glu	Arg	Lys	Lys
				85				90						95	
Arg	Arg	Ala	Glu	Ala	Glu	Glu	Met	Trp	Ile	Ala	Ala	Leu	Gln	Ala	Gly
			100					105					110		

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 Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro  
 130 135 140  
 Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala  
 145 150 155 160  
 Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu  
 165 170 175  
 Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys  
 180 185 190  
 Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile  
 195 200 205  
 Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln  
 210 215 220  
 Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val  
 225 230 235 240  
 Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly  
 245 250 255  
 Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val  
 260 265 270  
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr  
 275 280 285  
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu  
 290 295 300  
 Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu  
 305 310 315 320  
 Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe  
 325 330 335  
 Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe  
 340 345 350  
 Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala  
 355 360 365  
 Ala Cys Arg Gly Gly Arg Val His Arg Ala Pro Glu Pro Tyr Lys Ala  
 370 375 380  
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 385 390 395 400  
 Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro Pro Gly Asp Asp Pro  
 405 410 415  
 Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly  
 420 425 430  
 Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Glu Ala Gly Glu Arg  
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Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu Trp Gly Arg Leu Glu  
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 Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile  
 660 665 670  
 Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr Glu Thr Ala Ser Trp  
 675 680 685  
 Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro Leu Met Arg Arg Ala  
 690 695 700  
 Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg  
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 Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Gln Ala Phe Ile  
 725 730 735  
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 740 745 750  
 Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val Glu Thr Leu Phe Gly  
 755 760 765  
 Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg Val Lys Ser Val Arg  
 770 775 780

Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala  
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 Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Glu  
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 835 840 845  
 Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val  
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 865 870 875 880  
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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 569

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<210> 570

<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Synthetic

<400> 570

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<210> 571

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<212> DNA

<213> Artificial Sequence

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<210> 572

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 572

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Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
1           5           10           15
Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
20          25          30
Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
35          40          45
Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
50          55          60
Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65          70          75          80
Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
85          90          95
Leu Ile Lys Glu Met Val Asp Leu Leu Gly Leu Glu Arg Leu Glu Val
100         105         110
Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
115        120        125
Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu
130        135        140

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Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr  
145 150 155 160  
Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp  
165 170 175  
Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu  
180 185 190  
Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu  
195 200 205  
Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys  
210 215 220  
Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu  
225 230 235 240  
Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp  
245 250 255  
Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu  
260 265 270  
Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu  
275 280 285  
Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys  
290 295 300  
Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys  
305 310 315 320  
Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu  
325 330 335  
Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu  
340 345 350  
Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala  
355 360 365  
Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu  
370 375 380  
Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu  
385 390 395 400  
Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg  
405 410 415  
Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr  
420 425 430  
Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu  
435 440 445  
Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg  
450 455 460  
Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu  
465 470 475 480



Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu  
 485 490 495  
 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His  
 500 505 510  
 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser  
 515 520 525  
 Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr  
 530 535 540  
 Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn  
 545 550 555 560  
 Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val  
 565 570 575  
 Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu  
 580 585 590  
 Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val  
 595 600 605  
 Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe  
 610 615 620  
 Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys  
 625 630 635 640  
 Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser  
 645 650 655  
 Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg  
 660 665 670  
 Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu  
 675 680 685  
 Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg  
 690 695 700  
 Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala  
 705 710 715 720  
 Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp  
 725 730 735  
 Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met  
 740 745 750  
 Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala  
 755 760 765  
 Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met  
 770 775 780  
 Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met  
 785 790 795 800  
 Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His  
 805 810 815

<210> 573  
 <211> 2520  
 <212> DNA  
 <213> Artificial Sequence  
 <220>  
 <223> Synthetic

<400> 573  
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 gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct caaggaggac 180  
 ggggacgcgg tgatcgtggt ctttgacgcc aaggccccct ccttcgcgca cgaggcctac 240  
 ggggggtaca aggcgggccc ggccccacc ccggaggact tccccgcca gctcgccttg 300  
 gtcaagcggc tgggtggacct tctgggcctg gtccgcctcg agggcccggg gtacgaggcg 360  
 gacgacgtcc tgggcaccct ggccaagaag gccgaaaagg aggggtacga ggtgcgcatac 420  
 ctaccgcgcg accgcgacct ctaccaactc gtctccgacc gcatccacgt cctccacccc 480  
 gagggggtacc tcatcacccc ggagtggctt tgggagaagt atgggcttaa gccttcccag 540  
 tgggtggact accgggcctt ggccggggac ccttcgcaca acatccccgg cgtgaagggc 600  
 atcggggaga agacggcggc caagctgata cgggagtgga gaagcctgga aaacctctc 660  
 aagaacctgg accggctgaa gcccgccatc cgggagaaga tcttggccca catggacgat 720  
 ctgaagctct cctgggacct ggccaagggt cgcaccgacc tgccctgga ggtggacttc 780  
 gccaaaaggc gggagcccga ccgggagagg cttagggcct ttctggagag gcttgagttt 840  
 ggcagcctcc tccacgagtt cggccttctg gaaagcccca aggccttggga ggaggccccc 900  
 tggcccccgc cggaaggggc cttcgtgggc ttcgtcctct cccgccccga gcccatgtgg 960  
 gcggagctta aagccctggc cgcctgcagg ggcggccgcg tgcaccgggc agcagacccc 1020  
 ttggcggggc taaaggacct caaggaggtc cggggcctcc tcgccaagga cctcgcgcgc 1080  
 ttggcctcga gggaggggct agacctcgtg cccggggacg acccatgct cctcgcctac 1140  
 ctcttgacc cttcgaacac ccccccgag ggggtggcgc ggcgctacgg gggggagtgg 1200  
 acggaggacg ccgcccaccg ggccctctc tcggagaggc tccatcgga cctccttaag 1260  
 cgcctcgagg gggaggagaa gctcctttgg ctctaccacg aggtggaaaa gccctctcc 1320  
 cgggtcctgg cccatatgga ggccaccggg gtacggcggg acgtggccta ccttcaggcc 1380  
 ctttccttgg agcttgcgga ggagatccgc cgcctcgagg aggaggtctt ccgcttggcg 1440  
 ggccaccctc tcaacctcaa ctcccgggac cagctggaaa ggggtgctctt tgacgagctt 1500

aggcttcccc ccttgaagaa gacgaagaag acaggcaagc gctccaccag cgccgcggtg 1560  
 ctggaggccc tacgggaggg ccaccccatc gtggagaaga tcctccagca ccgggagctc 1620  
 accaagctca agaacaccta cgtggacccc ctcccaagcc tcgtccaccc gaggacgggc 1680  
 cgcctccaca cccgcttcaa ccagacggcc acggccacgg ggaggcttag tagctccgac 1740  
 cccaacctgc agaacatccc cgtccgcacc cccttgggcc agaggatccg ccgggccttc 1800  
 gtggccgagg cggttggggc gttggtggcc ctggactata gccagataga gctccgcgtc 1860  
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 cacaccaga ccgaagctg gatgttcggc gtccccccgg aggccgtgga cccctgatg 1980  
 cgccgggagg ccaagacggt gaacttcggc gtccctctacg gcatgtccgc ccataggctc 2040  
 tcccaggagc ttgccatccc ctacgaggag gcggtggcct ttatagagcg ctacttccaa 2100  
 agcttcccca aggtgcgggc ctggatagaa aagaccctgg aggaggggag gaagcggggc 2160  
 tacgtggaaa ccctcttcgg aagaaggcgc tacgtgcccg acctcaacgc ccgggtgaag 2220  
 agcgtcaggg aggccgcgga gcgcatggcc ttcaacatgc ccgtccaggg caccgccgcc 2280  
 gacctcatga agctcgccat ggtgaagctc ttccccgcc tccgggagat gggggcccg 2340  
 atgctcctcc aggtcgccaa cgagctcctc ctggaggccc cccaagcgcg ggccgaggag 2400  
 gtggcggcct tggccaagga ggccatggag aaggcctatc ccctcgccgt gcccctggag 2460  
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<210> 574

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 574

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
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Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val
	50					55					60				
Ile	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr
65					70					75				80	

Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg  
 85 90 95  
 Gln Leu Ala Leu Val Lys Arg Leu Val Asp Leu Leu Gly Leu Val Arg  
 100 105 110  
 Leu Glu Ala Pro Gly Tyr Glu Ala Asp Asp Val Leu Gly Thr Leu Ala  
 115 120 125  
 Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp  
 130 135 140  
 Arg Asp Leu Tyr Gln Leu Val Ser Asp Arg Ile His Val Leu His Pro  
 145 150 155 160  
 Glu Gly Tyr Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu  
 165 170 175  
 Lys Pro Ser Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser  
 180 185 190  
 Asp Asn Ile Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Ala Lys  
 195 200 205  
 Leu Ile Arg Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp  
 210 215 220  
 Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp  
 225 230 235 240  
 Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu  
 245 250 255  
 Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg  
 260 265 270  
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly  
 275 280 285  
 Leu Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro  
 290 295 300  
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp  
 305 310 315 320  
 Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg  
 325 330 335  
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly  
 340 345 350  
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp  
 355 360 365  
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro  
 370 375 380  
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp  
 385 390 395 400  
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg  
 405 410 415

Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr  
 420 425 430  
 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
 435 440 445  
 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu  
 450 455 460  
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala  
 465 470 475 480  
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
 485 490 495  
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly  
 500 505 510  
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His  
 515 520 525  
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys  
 530 535 540  
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly  
 545 550 555 560  
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
 565 570 575  
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu  
 580 585 590  
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu  
 595 600 605  
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
 610 615 620  
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile  
 625 630 635 640  
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val  
 645 650 655  
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
 660 665 670  
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr  
 675 680 685  
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
 690 695 700  
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly  
 705 710 715 720  
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn  
 725 730 735  
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
 740 745 750

Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val
		755					760					765			
Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln
	770					775					780				
Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	Glu	Glu
785					790					795				800	
Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	Leu	Ala
			805						810					815	
Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	Ser	Ala
		820						825					830		
Lys	Gly	His	His	His	His	His	His								
		835					840								

<210> 575

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 575

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caggcggtgt	acgggtttgc	caagagcctt	ttgaaggcgc	taaggggaaga	cggggatgtg	180
gtgatcgtgg	tgtttgacgc	caaggccccc	tccttcgcgc	accagacctt	cgaggcctac	240
aaggcggggc	gggctccccc	ccccgaggac	tttccccggc	agcttgccct	tatcaaggag	300
atggtggacc	ttttgggctt	taccgccttc	gaggtgccgc	gctttgaagc	ggatgacgtc	360
ctggctaccc	tggccaagaa	ggcggaaaag	gagggctacg	aggtccgcac	cctcaccgcc	420
gacaaagacc	tttaccagct	cctttccgac	cgcattccacg	tcctccaccc	cgaggggtac	480
ctcatcaccc	cggcctggct	ttgggaaaag	tacggcctga	ggcccgaaca	gtgggcccgc	540
taccgggccc	tgaccgggga	cgagtccgac	aaccttcccc	gggtcaaggg	catcggggag	600
aagacggcga	ggaagcttct	ggaggagtgg	gggagcctgg	aagccctcct	caagaacctg	660
gaccggctga	agcccgccat	ccgggagaag	atcctggccc	acatggacga	tctgaagctc	720
tcctgggacc	tggccaaggt	gcgcaccgac	ctgcccctgg	aggtggactt	cgccaaaagg	780
cgggagcccc	accgggaggg	ggagaagccc	cgggaggagg	ccccctggcc	cccggccgaa	840
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ctggccgcct	gcagggggcg	ccgcgtgcac	cgggcagcag	acccttggc	ggggctaaag	960

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gggctagacc tcgtgcccgg ggacgacccc atgctcctcg cctacctcct ggacctctcg	1080
aacaccacccc ccgaggggggt ggcgcggcgc tacggggggg agtggacgga ggacgccgcc	1140
caccggggccc tcctctcgga gaggtccat cggaacctcc ttaagcgctt cgagggggag	1200
gagaagctcc tttggctcta ccacgaggtg gaaaagcccc tctcccgggt cctggcccat	1260
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gcggaggaga tccgccgcct cgaggaggag gtcttccgct tggcgggcca ccccttcaac	1380
ctcaactccc gggaccagct ggaaagggtg ctctttgacg agcttaggct tcccgccttg	1440
aagaagacga agaagacagg caagcgctcc accagcgccg cgggtgctgga ggccctacgg	1500
gaggcccacc ccatcgtgga gaagatcctc cagcaccggg agctcaccaa gctcaagaac	1560
acctacgtgg accccctccc aagcctcgtc caccgagga cgggccgcct ccacaccgc	1620
ttcaaccaga cggccaaggc caccgggagg cttagtagct ccgaccccaa cctgcagaac	1680
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tgggcgttgg tggccctgga ctatagccag atagagctcc gcgtcctcgc ccacctctcc	1800
ggggacgaaa acctgatcag ggtcttccag gaggggaagg acatccacac ccagaccgca	1860
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cgggcctgga tagaaaagac cctggaggag gggaggaagc ggggctacgt ggaaaccctc	2100
ttcgaagaa ggcgctacgt gcccacctc aacgcccggg tgaagagcgt cagggaggcc	2160
gcggagcgca tggccttcaa catgcccgtc cagggcaccg ccgccgacct catgaagctc	2220
gccatggtga agctcttccc ccgcctccgg gagatggggg cccgcatgct cctccaggtc	2280
gccaacgagc tcctcctgga ggcccccaa gcgcgggccg aggaggtggc ggctttggcc	2340
aaggaggcca tggagaaggc ctatcccctc gccgtgcccc tggaggtgga ggtggggatg	2400
ggggaggact ggctttccgc caagggtcac caccaccacc accac	2445

<210> 576

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 576

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Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val
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Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly Leu
20      25      30
Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
35      40      45
Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Val Val Ile Val Val
50      55      60
Phe Asp Ala Lys Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr
65      70      75      80
Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
85      90      95
Leu Ile Lys Glu Met Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val
100     105     110
Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala
115     120     125
Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu
130     135     140
Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr
145     150     155     160
Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp
165     170     175
Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu
180     185     190
Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu
195     200     205
Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys
210     215     220
Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu
225     230     235     240
Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp
245     250     255
Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu
260     265     270
Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu
275     280     285
Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys
290     295     300
Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys
305     310     315     320

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Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu  
 325 330 335  
 Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu  
 340 345 350  
 Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala  
 355 360 365  
 Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu  
 370 375 380  
 Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu  
 385 390 395 400  
 Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg  
 405 410 415  
 Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr  
 420 425 430  
 Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu  
 435 440 445  
 Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg  
 450 455 460  
 Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu  
 465 470 475 480  
 Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu  
 485 490 495  
 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His  
 500 505 510  
 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser  
 515 520 525  
 Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn Gln Thr  
 530 535 540  
 Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu Gln Asn  
 545 550 555 560  
 Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala Phe Val  
 565 570 575  
 Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln Ile Glu  
 580 585 590  
 Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile Arg Val  
 595 600 605  
 Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe  
 610 615 620  
 Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys  
 625 630 635 640  
 Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser  
 645 650 655

Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg  
                   660                                  665                                  670  
 Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys Thr Leu  
                   675                                  680                                  685  
 Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly Arg Arg  
                   690                                  695                                  700  
 Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala  
                   705                                  710                                  715                                  720  
 Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp  
                   725                                  730                                  735  
 Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met  
                   740                                  745                                  750  
 Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala  
                   755                                  760                                  765  
 Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met  
                   770                                  775                                  780  
 Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val Gly Met  
                   785                                  790                                  795                                  800  
 Gly Glu Asp Trp Leu Ser Ala Lys Gly His His His His His His  
                   805                                  810                                  815

<210> 577

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 577

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gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct caaggaggac	180
ggggacgcgg tgatcgtggt ctttgacgcc aaggccccct cttccgccca cgaggcctac	240
gggggggtaca aggcggggccg ggccccacc ccggaggact tccccgccca gctcgccttg	300
gtcaagcggc tgggtggacct tctgggcttt accgcctcg aggccccggg gtacgaggcg	360
gacgacgtcc tgggcaccct ggccaagaag gccgaaaagg aggggtacga ggtgcgcac	420
ctcaccgccg accgcgacct ctaccaactc gtctccgacc gcatccacgt cctccacccc	480
gaggggtacc tcatcacccc ggagtggctt tgggagaagt atgggcttaa gccttcccag	540
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atcggggaga agacggcggc caagctgata cgggagtggg gaagcctgga aaacctcctc	660
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<210> 578

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 578

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			20					25						30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	
		35					40					45				
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	
	50					55					60					
Ile	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	
65					70					75					80	
Gly	Gly	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	
			85						90					95		
Gln	Leu	Ala	Leu	Val	Lys	Arg	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	
			100					105					110			
Leu	Glu	Ala	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Gly	Thr	Leu	Ala	
		115					120					125				
Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	
	130					135					140					
Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	
145					150					155					160	
Glu	Gly	Tyr	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	
			165					170						175		
Lys	Pro	Ser	Gln	Trp	Val	Asp	Tyr	Arg	Ala	Leu	Ala	Gly	Asp	Pro	Ser	
			180					185					190			
Asp	Asn	Ile	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Ala	Lys	
	195						200					205				
Leu	Ile	Arg	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	Asp	
	210					215					220					

Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp  
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 Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu  
 245 250 255  
 Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg  
 260 265 270  
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly  
 275 280 285  
 Leu Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro  
 290 295 300  
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp  
 305 310 315 320  
 Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg  
 325 330 335  
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly  
 340 345 350  
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp  
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 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro  
 370 375 380  
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp  
 385 390 395 400  
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg  
 405 410 415  
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr  
 420 425 430  
 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
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 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu  
 450 455 460  
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 465 470 475 480  
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
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 Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly  
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 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His  
 515 520 525  
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys  
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 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly  
 545 550 555 560

Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
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 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu  
 580 585 590  
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu  
 595 600 605  
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
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 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile  
 625 630 635 640  
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val  
 645 650 655  
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
 660 665 670  
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr  
 675 680 685  
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
 690 695 700  
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly  
 705 710 715 720  
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn  
 725 730 735  
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
 740 745 750  
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val  
 755 760 765  
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln  
 770 775 780  
 Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu  
 785 790 795 800  
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala  
 805 810 815  
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala  
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 Lys Gly His His His His His His  
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<210> 579

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 579

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aagacggcga ggaagcttct ggaggagtgg gggagcctgg aagccctcct caagaacctg    660
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<210> 580

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 580

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Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu
			20					25					30		
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
		35					40					45			
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val
	50					55					60				
Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr
65					70					75				80	
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
			85						90					95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Leu	Glu	Arg	Leu	Glu	Val
			100					105						110	



Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala  
 115 120 125  
 Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp Leu  
 130 135 140  
 Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr  
 145 150 155 160  
 Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp  
 165 170 175  
 Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu  
 180 185 190  
 Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu  
 195 200 205  
 Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys  
 210 215 220  
 Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu  
 225 230 235 240  
 Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val Asp  
 245 250 255  
 Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Glu Lys Pro Arg Glu  
 260 265 270  
 Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Phe Leu Leu  
 275 280 285  
 Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Lys Ala Leu Ala Ala Cys  
 290 295 300  
 Arg Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly Leu Lys  
 305 310 315 320  
 Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala Val Leu  
 325 330 335  
 Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro Met Leu  
 340 345 350  
 Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly Val Ala  
 355 360 365  
 Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg Ala Leu  
 370 375 380  
 Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu Gly Glu  
 385 390 395 400  
 Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu Ser Arg  
 405 410 415  
 Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val Ala Tyr  
 420 425 430  
 Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg Leu Glu  
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Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn Ser Arg  
 450 455 460  
 Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro Ala Leu  
 465 470 475 480  
 Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala Val Leu  
 485 490 495  
 Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu Gln His  
 500 505 510  
 Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu Pro Ser  
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 Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp Met Phe  
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 Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala Ala Lys  
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 Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg Leu Ser  
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 Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile Glu Arg  
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 Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg Glu Ala  
 705 710 715 720  
 Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala Ala Asp  
 725 730 735  
 Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg Glu Met  
 740 745 750  
 Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu Glu Ala  
 755 760 765

Pro	Gln	Ala	Arg	Ala	Glu	Glu	Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met
770						775					780				
Glu	Lys	Ala	Tyr	Pro	Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met
785					790					795					800
Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Gly	His	His	His	His	His	His	His
				805					810						815

<210> 581

<211> 2445

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 581

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ggggacgaaa acctgatcag ggtcttccag gagggggaagg acatccacac ccagaccgca 1860  
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gccaacgagc tcctcctgga ggccccccaa gcgcggggcg aggaggtggc ggctttggcc 2340  
aaggaggcca tggagaaggc ctatcccctc gccgtgcccc tggaggtgga ggtggggatg 2400  
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<210> 582

<211> 815

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 582

Met	Asn	Ser	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val
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Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly	Leu
			20					25					30		

Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
		35					40					45			
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val
	50					55					60				
Phe	Asp	Ala	Glu	Ala	Pro	Ser	Phe	Arg	His	Gln	Thr	Tyr	Glu	Ala	Tyr
65					70					75					80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
				85					90					95	
Leu	Ile	Lys	Glu	Met	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu	Glu	Val
			100					105					110		
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala
		115					120						125		
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Lys	Asp	Leu
	130					135					140				
Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	Glu	Gly	Tyr
145					150					155					160
Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg	Pro	Asp
				165					170					175	
Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	Asp	Asn	Leu
			180					185						190	
Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	Leu	Leu	Glu
		195					200					205			
Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	Arg	Leu	Lys
	210					215					220				
Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	Leu	Lys	Leu
225					230					235					240
Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	Glu	Val	Asp
				245					250					255	
Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Glu	Lys	Pro	Arg	Glu
			260					265					270		
Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Leu	Leu
		275					280					285			
Ser	Arg	Pro	Glu	Pro	Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys
	290					295					300				
Arg	Gly	Gly	Arg	Val	His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys
305					310					315					320
Asp	Leu	Lys	Glu	Val	Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu
				325					330					335	
Ala	Ser	Arg	Glu	Gly	Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu
			340					345					350		
Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala
		355					360					365			

Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu
370						375					380				
Leu	Ser	Glu	Arg	Leu	His	Arg	Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu
385					390					395					400
Glu	Lys	Leu	Leu	Trp	Leu	Tyr	His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg
				405					410					415	
Val	Leu	Ala	His	Met	Glu	Ala	Thr	Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr
			420					425					430		
Leu	Gln	Ala	Leu	Ser	Leu	Glu	Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu
		435					440					445			
Glu	Glu	Val	Phe	Arg	Leu	Ala	Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg
	450					455					460				
Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu
465					470					475					480
Lys	Lys	Thr	Lys	Lys	Thr	Gly	Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu
				485					490					495	
Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His
			500					505					510		
Arg	Glu	Leu	Thr	Lys	Leu	Lys	Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser
		515					520					525			
Leu	Val	His	Pro	Arg	Thr	Gly	Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr
	530					535					540				
Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn
545					550					555					560
Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val
				565				570						575	
Ala	Glu	Ala	Gly	Trp	Ala	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu
			580					585					590		
Leu	Arg	Val	Leu	Ala	His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val
		595					600					605			
Phe	Gln	Glu	Gly	Lys	Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe
	610					615					620				
Gly	Val	Pro	Pro	Glu	Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys
625					630					635					640
Thr	Val	Asn	Phe	Gly	Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser
				645					650					655	
Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg
			660					665					670		
Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu
		675					680					685			
Glu	Glu	Gly	Arg	Lys	Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg
	690					695					700				

Arg	Tyr	Val	Pro	Asp	Leu	Asn	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala
705					710					715					720
Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp
				725					730						735
Leu	Met	Lys	Leu	Ala	Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met
			740					745						750	
Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	Ala	Asn	Glu	Leu	Leu	Leu	Glu	Ala
		755					760							765	
Pro	Gln	Ala	Arg	Ala	Glu	Glu	Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met
		770					775					780			
Glu	Lys	Ala	Tyr	Pro	Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met
785					790					795					800
Gly	Glu	Asp	Trp	Leu	Ser	Ala	Lys	Gly	His	His	His	His	His	His	His
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<210> 583

<211> 2520

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 583

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gagccggtcc aggcggtgta cgggtttgcc aagagccttt tgaaggcgct aagagaagac	180
ggggacgcgg tgatcggtgt ctttgacgcc gagggcccct ccttcgccca cgaggcctac	240
gggggggtaca aggcggggcg ggctcccacc cccgaggact ttccccggca gcttgccctt	300
atcaaggagc tgggtggacct cctgggggttt accgcctcag aggtccccgg ctacgaggcg	360
gacgacgttc tcgccaccct ggccaagaag gcggaagagg aggggtacga ggtgcgcac	420
ctcaccgccg acaaagacct ttaccagctc ctttcgcacc gcatccacgt cctccacccc	480
gaggggtacc tcatcacccc ggcttggttt tgggaaaagt acggcctgag gcccgaccag	540
tgggcccact accggggcct gaccggggac gaggccgaca accttcgccg ggtcaagggc	600
atcggggaga agaccgccct caagctctc aaggagtggg ggagcctgga agccctctc	660
aagaacctgg accggctgaa gcccgccatc cgggagaaga tcctggccca catggacgat	720
ctgaagctct cctgggacct ggccaagggt cgcaccgacc tgcccctgga ggtggacttc	780
gccaaaaggc gggagcccga ccgggagggg cttaaggcct ttttgagag gctggagttc	840

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cacaccacga	ccgcaagctg	gatgttcggc	gtcccccccg	aggccgtgga	ccccctgatg	1980
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gtggcggtct	tggccaagga	ggccatggag	aaggcctatc	ccctcgccgt	gcccctggag	2460
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<210> 584

<211> 840

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 584

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Leu Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu  
20 25 30  
Lys Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly  
35 40 45  
Phe Ala Lys Ser Leu Leu Lys Ala Leu Arg Glu Asp Gly Asp Ala Val  
50 55 60  
Ile Val Val Phe Asp Ala Glu Ala Pro Ser Phe Arg His Glu Ala Tyr  
65 70 75 80  
Gly Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg  
85 90 95  
Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg  
100 105 110  
Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala  
115 120 125  
Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp  
130 135 140  
Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro  
145 150 155 160  
Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu  
165 170 175  
Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser  
180 185 190  
Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys  
195 200 205  
Leu Leu Lys Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp  
210 215 220  
Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp  
225 230 235 240  
Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu  
245 250 255

Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Gly Leu Lys  
 260 265 270  
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly  
 275 280 285  
 Leu Leu Gly Gly Glu Lys Pro Arg Glu Glu Ala Pro Trp Pro Pro Pro  
 290 295 300  
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp  
 305 310 315 320  
 Ala Asp Leu Leu Ala Leu Ala Ala Cys Arg Gly Gly Arg Val His Arg  
 325 330 335  
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly  
 340 345 350  
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp  
 355 360 365  
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro  
 370 375 380  
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp  
 385 390 395 400  
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg  
 405 410 415  
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr  
 420 425 430  
 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala  
 435 440 445  
 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu  
 450 455 460  
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala  
 465 470 475 480  
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu  
 485 490 495  
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly  
 500 505 510  
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His  
 515 520 525  
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys  
 530 535 540  
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly  
 545 550 555 560  
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu  
 565 570 575  
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu  
 580 585 590

Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu  
 595 600 605  
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu  
 610 615 620  
 Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile  
 625 630 635 640  
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val  
 645 650 655  
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu  
 660 665 670  
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr  
 675 680 685  
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys  
 690 695 700  
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly  
 705 710 715 720  
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn  
 725 730 735  
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn  
 740 745 750  
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val  
 755 760 765  
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln  
 770 775 780  
 Val Ala Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu  
 785 790 795 800  
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala  
 805 810 815  
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala  
 820 825 830  
 Lys Gly His His His His His His  
 835 840

<210> 585

<211> 2499

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 585

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cagatggtct	acggcttcgc	ccggagcctc	ctcaaggcct	tgaaggagga	cggacaggcg	180
gtggtcgtgg	tctttgacgc	caaggccccc	tccttccgcc	acgaggccta	cgaggcctac	240
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 gaggtgggga tgggggagga ctggctttcc gccaagggt 2499

<210> 586

<211> 811

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 586

Met	Glu	Phe	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val
1				5					10					15	
Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	Gly	Leu
			20					25					30		
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
		35					40					45			
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val
	50					55					60				
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	Gly	Tyr
65					70					75					80
Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln	Leu	Ala
				85					90					95	
Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	Leu	Glu	Val
			100					105					110		
Pro	Gly	Phe	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys	Lys	Ala
		115					120					125			
Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Gly	Asp	Arg	Asp	Leu
	130					135					140				

Tyr Gln Leu Val Ser Asp Arg Val Ala Arg Pro Glu Gln Trp Val Asp  
 145 150 155 160  
 Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile Pro Gly Val Lys  
 165 170 175  
 Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp Gly Ser  
 180 185 190  
 Val Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala Ile Arg  
 195 200 205  
 Glu Lys Ile Leu Ala His Met Glu Asp Leu Lys Leu Ser Leu Glu Leu  
 210 215 220  
 Ser Arg Val Arg Thr Asp Leu Pro Leu Glu Val Asp Leu Ala Gln Gly  
 225 230 235 240  
 Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe Leu Glu Arg Leu Glu  
 245 250 255  
 Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro Val Ala  
 260 265 270  
 Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Tyr  
 275 280 285  
 Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Asn Ala Leu Ala  
 290 295 300  
 Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly  
 305 310 315 320  
 Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala  
 325 330 335  
 Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro  
 340 345 350  
 Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly  
 355 360 365  
 Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg  
 370 375 380  
 Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu  
 385 390 395 400  
 Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu  
 405 410 415  
 Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val  
 420 425 430  
 Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg  
 435 440 445  
 Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn  
 450 455 460  
 Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro  
 465 470 475 480

Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala  
 485 490 495  
 Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu  
 500 505 510  
 Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu  
 515 520 525  
 Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn  
 530 535 540  
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu  
 545 550 555 560  
 Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala  
 565 570 575  
 Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln  
 580 585 590  
 Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile  
 595 600 605  
 Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp  
 610 615 620  
 Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala  
 625 630 635 640  
 Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg  
 645 650 655  
 Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile  
 660 665 670  
 Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys  
 675 680 685  
 Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly  
 690 695 700  
 Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg  
 705 710 715 720  
 Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala  
 725 730 735  
 Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg  
 740 745 750  
 Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu  
 755 760 765  
 Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu  
 770 775 780  
 Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val  
 785 790 795 800  
 Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly  
 805 810

<210> 587

<211> 2433

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 587

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caggcgggtgt acgggtttgc caagagcctt ttgaaggcgc taagagaaga cggggatgtg	180
gtgatcgtgg tctttgacgc caaggcccc tccttcgcc acgaggccta cggggggtac	240
aaggcggggc gggccccgac ccccgaggac tcccccggc agctcgccct catcaaggag	300
ctggtggacc tcttggggct ggcgcgcctc gaggtgccgg gctttgaagc ggatgacgtc	360
ctggctaccc tggccaagaa ggcggaagaa gagggctacg aggtgcgcat tctcacgggc	420
gaccgcgacc tttaaccaact cgtctccgac cgcgtcgcca ggccggagca gtgggtggac	480
taccgggcct tggccgggga cccttcgac aacatccccg gcgtgaaggg catcggggag	540
aagacggcga ggaagcttct ggaggagtgg gggagcgtgg aagccctcct caagaacctg	600
gaccggctga agcccgccat ccgggagaag atcctggccc acatggagga cctcaagcta	660
tccctggagc tatcccggtt gcgcaccgac ctccccctgg aggtggacct cgcccagggg	720
cgggagcccc accgggaggg gcttaaggcc tttttggaga ggctggagtt cggaagcctc	780
ctccacgagt tcggcctgtt ggaaagcccc gtggcgggcg aggaagctcc ctggccgccc	840
cccgagggag ccttcgtggg gtacgttctt tcccgcctcg agcccatgtg ggcggagctt	900
aacgccttgg ccgcgcctg gggcgggcgc gtgcaccggg cagcagacct cttggcgggg	960
ctaaaggacc tcaaggaggt ccggggcctc ctgcgaagg acctcgccgt cttggcctcg	1020
agggaggggc tagacctcgt gcccggggac gacccatgc tcctcgcta cctcctggac	1080
ccttcgaaca ccacccccga gggggtggcg cggcgctacg ggggggagtg gacggaggac	1140
gccgcccacc gggccctcct ctcgagaggg ctccatcgga acctcctaa gcgcctcgag	1200
ggggaggaga agctcctttg gctctaccac gaggtggaaa agccctctc cggggtcctg	1260
gcccataatg aggccaccgg ggtacggcgg gacgtggcct accttcaggc cctttccctg	1320
gagcttgccg aggagatccg ccgcctcgag gaggaggtct tccgcttggc gggccacccc	1380
ttcaacctca actcccggga ccagctggaa aggggtgctct ttgacgagct taggcttccc	1440
gccttgaaga agacgaagaa gacaggcaag cgctccacca gcgccgcggt gctggaggcc	1500



ctacgggagg cccaccccat cgtggagaag atcctccagc accgggagct caccaagctc 1560  
aagaacacct acgtggaccc cctcccaagc ctcgtccacc cgaggacggg ccgcctccac 1620  
acccgcttca accagacggc cacggccacg gggaggctta gtagctccga cccaacctg 1680  
cagaacatcc ccgtccgcac ccccttgggc cagaggatcc gccgggcctt cgtggccgag 1740  
gcgggttggg cgttggtggc cctggactat agccagatag agctccgcgt cctcgccac 1800  
ctctccgggg acgaaaacct gatcagggtc ttccaggagg ggaaggacat ccacaccag 1860  
accgcaagct ggatgttcgg cgtcccccg gaggcgtgg accccctgat gcgccgggag 1920  
gccaagacgg tgaacttcgg cgtcctctac ggcatgtccg cccataggct ctcccaggag 1980  
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accctcttcg gaagaaggcg ctacgtgccg gacctcaacg cccgggtgaa gagcgtcagg 2160  
gagggcgcgg agcgcattggc cttcaacatg cccgtccagg gcaccgccgc cgacctcatg 2220  
aagctcgcca tggatgaagct cttccccgc ctccgggaga tgggggccc catgctctc 2280  
caggtcgcca acgagctcct cctggaggcc cccaagcgc gggccgagga ggtggcggt 2340  
ttggccaagg aggccatgga gaaggcctat cccctcgccg tgcccctgga ggtggagggtg 2400  
gggatggggg aggactggct ttccgccaag ggt 2433

<210> 588

<211> 811

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 588

Met	Glu	Phe	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val
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Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	Gly	Leu
			20					25					30		
Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys
		35				40					45				
Ser	Leu	Leu	Lys	Ala	Leu	Arg	Glu	Asp	Gly	Asp	Val	Val	Ile	Val	Val
	50					55					60				
Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	Gly	Tyr
65					70					75				80	

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala  
 85 90 95  
 Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu Val  
 100 105 110  
 Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala  
 115 120 125  
 Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Gly Asp Arg Asp Leu  
 130 135 140  
 Tyr Gln Leu Val Ser Asp Arg Val Ala Arg Pro Glu Gln Trp Val Asp  
 145 150 155 160  
 Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile Pro Gly Val Lys  
 165 170 175  
 Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu Glu Trp Gly Ser  
 180 185 190  
 Val Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys Pro Ala Ile Arg  
 195 200 205  
 Glu Lys Ile Leu Ala His Met Glu Asp Leu Lys Leu Ser Leu Glu Leu  
 210 215 220  
 Ser Arg Val Arg Thr Asp Leu Pro Leu Glu Val Asp Leu Ala Gln Gly  
 225 230 235 240  
 Arg Glu Pro Asp Arg Glu Gly Leu Lys Ala Phe Leu Glu Arg Leu Glu  
 245 250 255  
 Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu Ser Pro Val Ala  
 260 265 270  
 Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala Phe Val Gly Tyr  
 275 280 285  
 Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu Asn Ala Leu Ala  
 290 295 300  
 Ala Ala Trp Gly Gly Arg Val His Arg Ala Ala Asp Pro Leu Ala Gly  
 305 310 315 320  
 Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu Ala Lys Asp Leu Ala  
 325 330 335  
 Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro Gly Asp Asp Pro  
 340 345 350  
 Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr Thr Pro Glu Gly  
 355 360 365  
 Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp Ala Ala His Arg  
 370 375 380  
 Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu Leu Lys Arg Leu Glu  
 385 390 395 400  
 Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu Val Glu Lys Pro Leu  
 405 410 415

Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val Arg Arg Asp Val  
 420 425 430  
 Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu Glu Ile Arg Arg  
 435 440 445  
 Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro Phe Asn Leu Asn  
 450 455 460  
 Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu Leu Arg Leu Pro  
 465 470 475 480  
 Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser Thr Ser Ala Ala  
 485 490 495  
 Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val Glu Lys Ile Leu  
 500 505 510  
 Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr Val Asp Pro Leu  
 515 520 525  
 Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His Thr Arg Phe Asn  
 530 535 540  
 Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp Pro Asn Leu  
 545 550 555 560  
 Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg Ile Arg Arg Ala  
 565 570 575  
 Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu Asp Tyr Ser Gln  
 580 585 590  
 Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp Glu Asn Leu Ile  
 595 600 605  
 Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln Thr Ala Ser Trp  
 610 615 620  
 Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu Met Arg Arg Ala  
 625 630 635 640  
 Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met Ser Ala His Arg  
 645 650 655  
 Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala Val Ala Phe Ile  
 660 665 670  
 Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala Trp Ile Glu Lys  
 675 680 685  
 Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu Thr Leu Phe Gly  
 690 695 700  
 Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val Lys Ser Val Arg  
 705 710 715 720  
 Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val Gln Gly Thr Ala  
 725 730 735  
 Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe Pro Arg Leu Arg  
 740 745 750

Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn Glu Leu Leu Leu  
 755 760 765  
 Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala Leu Ala Lys Glu  
 770 775 780  
 Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu Glu Val Glu Val  
 785 790 795 800  
 Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly  
 805 810

<210> 589

<211> 2493

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 589

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ctggcctacc gtacctttt tgccctgaag ggccctacca cctcccgggg ggagccggtg	120
cagatggtct acggcttcgc ccggagcctc ctcaaggccc tcaaggagga cggggacgcg	180
gtgatcgtgg tctttgacgc cgaggccccc tccttcgcc accagacctt cgaggcctac	240
aaggcgggga gggctccacc ccccgaggac tttcccgggc agcttgccct tatcaaggag	300
ctggtggacc tcctgggggt taccgcctc gaggtccccg gctacgaggc ggacgacgtt	360
ctcgccaccc tggccaagaa ggcggaagaa gagggctacg aggtgcgcac cctcaccgcg	420
gaccgggacc tttaccagct tctttccgac cgcattcacg tccttcaccc cgaggggtac	480
ctcatcacc cggcctggct ttgggaaaag tacggcttga ggcccagca gtgggcccac	540
taccgggccc tgaccgggga cgaatccgac aacctttccg gggtaaggga catcggggag	600
aagacggcga ggaagcttct ggaggagtgg gggagcctgg aagccctcct caagaacctg	660
gaccggctga agcccgccat ccgggagaag atcctggccc acatggacga tctgaagctc	720
tccttgagac tctcccgggt gcgcaccgac ctccccctgg aggtggactt cgccaaaagg	780
cgggagcccc accgggagag gcttagggcc tttctggaga ggcttgagtt tggcagcctc	840
ctccacgagt tcggcccttt ggaaagcccc agggccgagg aggaagctcc ctggccgccc	900
cccaggggag ccttcgtggg gtacgttctt tcccggccc agcccatgtg ggcggagctt	960
aacgccttgg ccgcccag gggcgccgc gtgcaccggg cagcagaccc cttggcgggg	1020
ctaaaggacc tcaaggaggt ccggggcctc ctgcaccaag acctcgccgt cttggcctcg	1080
agggaggggc tagacctcgt gccgggggac gaccccatgc tcctcgcta cctcctggac	1140

ccttcgaaca ccacccccga gggggtggcg cggcgctacg ggggggagtg gacggaggac	1200
gccgcccacc gggccctcct ctccgagagg ctccatcgga acctccttaa gcgcctcgag	1260
ggggaggaga agctcctttg gctctaccac gaggtggaaa agccccctctc ccgggtcctg	1320
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gagcttgccg aggagatccg ccgcctcgag gaggaggtct tccgcttggc gggccacccc	1440
ttcaacctca actcccggga ccagctggaa aggggtgctct ttgacgagct taggcttccc	1500
gccttgaaga agacgaagaa gacaggcaag cgctccacca gcgccgcggt gctggaggcc	1560
ctacgggagg cccacccccat cgtggagaag atcctccagc accgggagct caccaagctc	1620
aagaacacct acgtggaccc cctcccaagc ctcgctccacc cgaggacggg ccgcctccac	1680
accgccttca accagacggc cacggccacg gggaggctta gtagctccga cccaacctg	1740
cagaacatcc ccgtccgcac ccccttgggc cagaggatcc gccgggcctt cgtggccgag	1800
gcgggttggg cgttggtggc cctggactat agccagatag agctccgcgt cctcgcccac	1860
ctctccgggg acgaaaacct gatcagggtc ttccaggagg ggaaggacat ccacaccag	1920
accgcaagct ggatgttcgg cgtccccccg gaggcctgg accccctgat gcgccgggcg	1980
gccaaagacgg tgaacttcgg cgtcctctac ggcatgtccg cccataggct ctcccaggag	2040
cttgccatcc cctacgagga ggcggtggcc tttatagagc gctacttcca aagcttcccc	2100
aaggtgcggg cctggataga aaagaccctg gaggagggga ggaagcgggg ctacgtggaa	2160
accctcttcg gaagaaggcg ctacgtgcc gacctcaacg cccgggtgaa gagcgtcagg	2220
gaggccgcgg agcgcattgg cttcaacatg cccgtccagg gcaccgccgc cgacctcatg	2280
aagctcgcca tggatgaagct cttccccgc ctccgggaga tggggggccg catgctctc	2340
caggctcgcca acgagctcct cctggaggcc cccaagcgc gggccgagga ggtggcggct	2400
ttggccaagg aggccatgga gaaggcctat cccctcgccg tgcccctgga ggtggagggtg	2460
gggatggggg aggactggct ttccgccaag ggt	2493

<210> 590

<211> 831

<212> PRT

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 590

Met Asn Ser Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val  
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20 25 30  
Thr Thr Ser Arg Gly Glu Pro Val Gln Met Val Tyr Gly Phe Ala Arg  
35 40 45  
Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val  
50 55 60  
Phe Asp Ala Glu Ala Pro Ser Phe Arg His Gln Thr Tyr Glu Ala Tyr  
65 70 75 80  
Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala  
85 90 95  
Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu Glu Val  
100 105 110  
Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys Ala  
115 120 125  
Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu  
130 135 140  
Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly Tyr  
145 150 155 160  
Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro Asp  
165 170 175  
Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn Leu  
180 185 190  
Ser Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu Glu  
195 200 205  
Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu Lys  
210 215 220  
Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys Leu  
225 230 235 240  
Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu Glu Val Asp  
245 250 255  
Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe Leu  
260 265 270  
Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Pro Leu Glu  
275 280 285  
Ser Pro Arg Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala  
290 295 300  
Phe Val Gly Tyr Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu Leu  
305 310 315 320

Asn Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Ala Asp  
 325 330 335  
 Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly Leu Leu Ala  
 340 345 350  
 Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp Leu Val Pro  
 355 360 365  
 Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr  
 370 375 380  
 Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp  
 385 390 395 400  
 Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg Asn Leu Leu  
 405 410 415  
 Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr His Glu Val  
 420 425 430  
 Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly Val  
 435 440 445  
 Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Leu Ala Glu  
 450 455 460  
 Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro  
 465 470 475 480  
 Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu  
 485 490 495  
 Leu Arg Leu Pro Ala Leu Lys Lys Thr Lys Lys Thr Gly Lys Arg Ser  
 500 505 510  
 Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val  
 515 520 525  
 Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys Asn Thr Tyr  
 530 535 540  
 Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly Arg Leu His  
 545 550 555 560  
 Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser Ser  
 565 570 575  
 Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln Arg  
 580 585 590  
 Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu Val Ala Leu  
 595 600 605  
 Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly Asp  
 610 615 620  
 Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile His Thr Gln  
 625 630 635 640  
 Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro Leu  
 645 650 655

Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu Tyr Gly Met  
 660 665 670  
 Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu Ala  
 675 680 685  
 Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg Ala  
 690 695 700  
 Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly Tyr Val Glu  
 705 710 715 720  
 Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg Val  
 725 730 735  
 Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro Val  
 740 745 750  
 Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu Phe  
 755 760 765  
 Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln Val Ala Asn  
 770 775 780  
 Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu Val Ala Ala  
 785 790 795 800  
 Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala Val Pro Leu  
 805 810 815  
 Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala Lys Gly  
 820 825 830

<210> 591

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic

<400> 591

agaaaggaag ggaagaaagc gaa

23

<210> 592

<211> 45

<212> DNA

<213> Artificial Sequence

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